

Fig. 1

5'	9			18			27			36			45			54		
	GTG	GGC	ATG	GTG	GGC	AAC	GTC	CTG	CTG	GTG	CTG	GTG	ATC	GCG	CGG	GTG	CGC	CGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Val	Gly	Met	Val	Gly	Asn	Val	Leu	Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg
	63			72			81			90			99			108		
	CTG	CAC	AAC	GTG	ACG	AAC	TTC	CTC	ATC	GGC	AAC	CTG	GCC	TTG	TCC	GAC	GTG	CTC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	His	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu
	117			126			135			144			153			162		
	ATG	TGC	ACC	GCC	TGC	GTG	CCG	CTC	ACG	CTG	GCC	TAT	GCC	TTC	GAG	CCA	CGC	GGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly
	171			180			189			198			207			216		
	TGG	GTG	TTC	GGC	GGC	GGC	CTG	TGC	CAC	CTG	GTC	TTC	TTC	CTG	CAG	CCG	GTC	ACC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Trp	Val	Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	225			234			243			252			261			270		
	GTC	TAT	GTG	TCG	GTG	TTC	ACG	CTC	ACC	ACC	ATC	GCA	GTG	GAC	CGG	TAC	GTC	GTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val
	279			288			297											
	CTG	GTG	CAC	CCG	CTG	AGG	CGG	CGC	ATC	3'								
	---	---	---	---	---	---	---	---	---									
	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile									

Fig. 2

5' 9 18 27 36 45 54
 GGC CTG CTG CTG GTC ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr

 63 72 81 90 99 108
 GTC CGG GTG TCA GTG AAG CTC CGC AAC CGC GTG GTG CCG GGC TGC GTG ACC CAG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Cys Val Thr Gln

 117 126 135 144 153 162
 AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val

 171 180 189 198
 GTG GTC GTG GTG GTG TTT GCC ATC TGC TGG TTG CCT TAC TAC 3'
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr

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Fig. 3

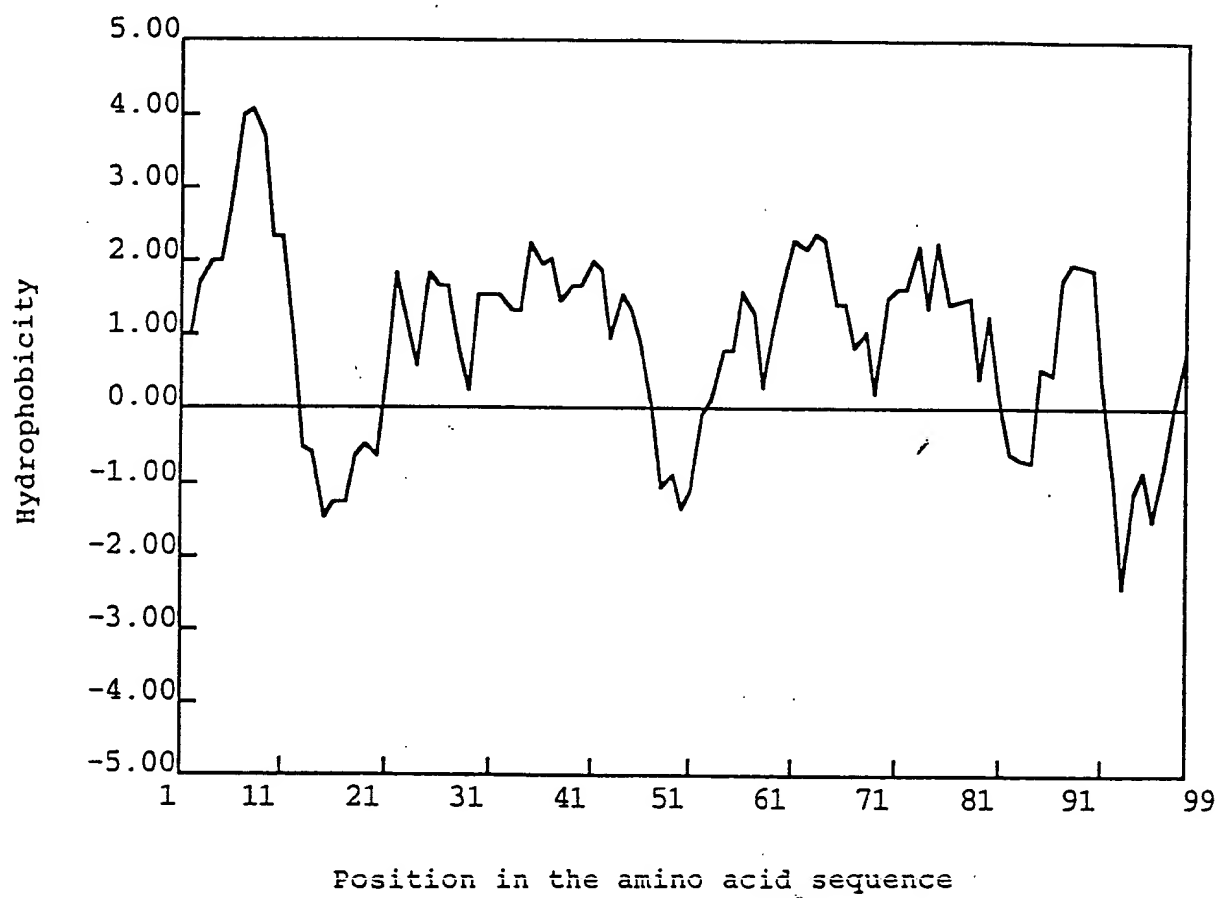
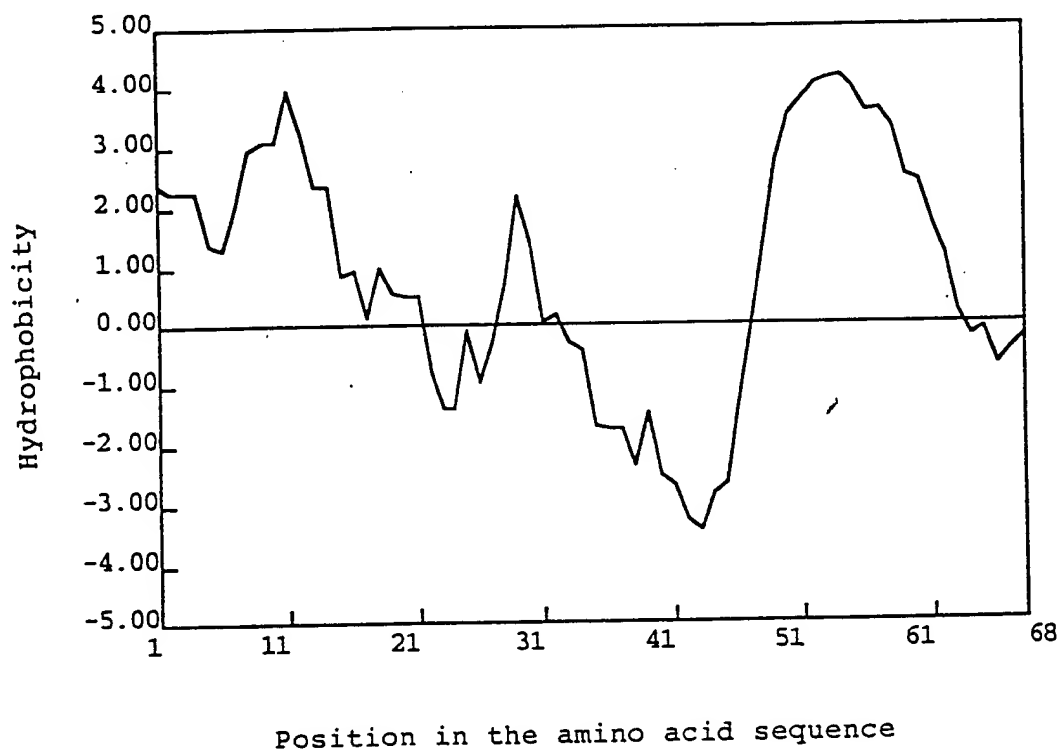


Fig. 4



[illegible]

Fig. 6

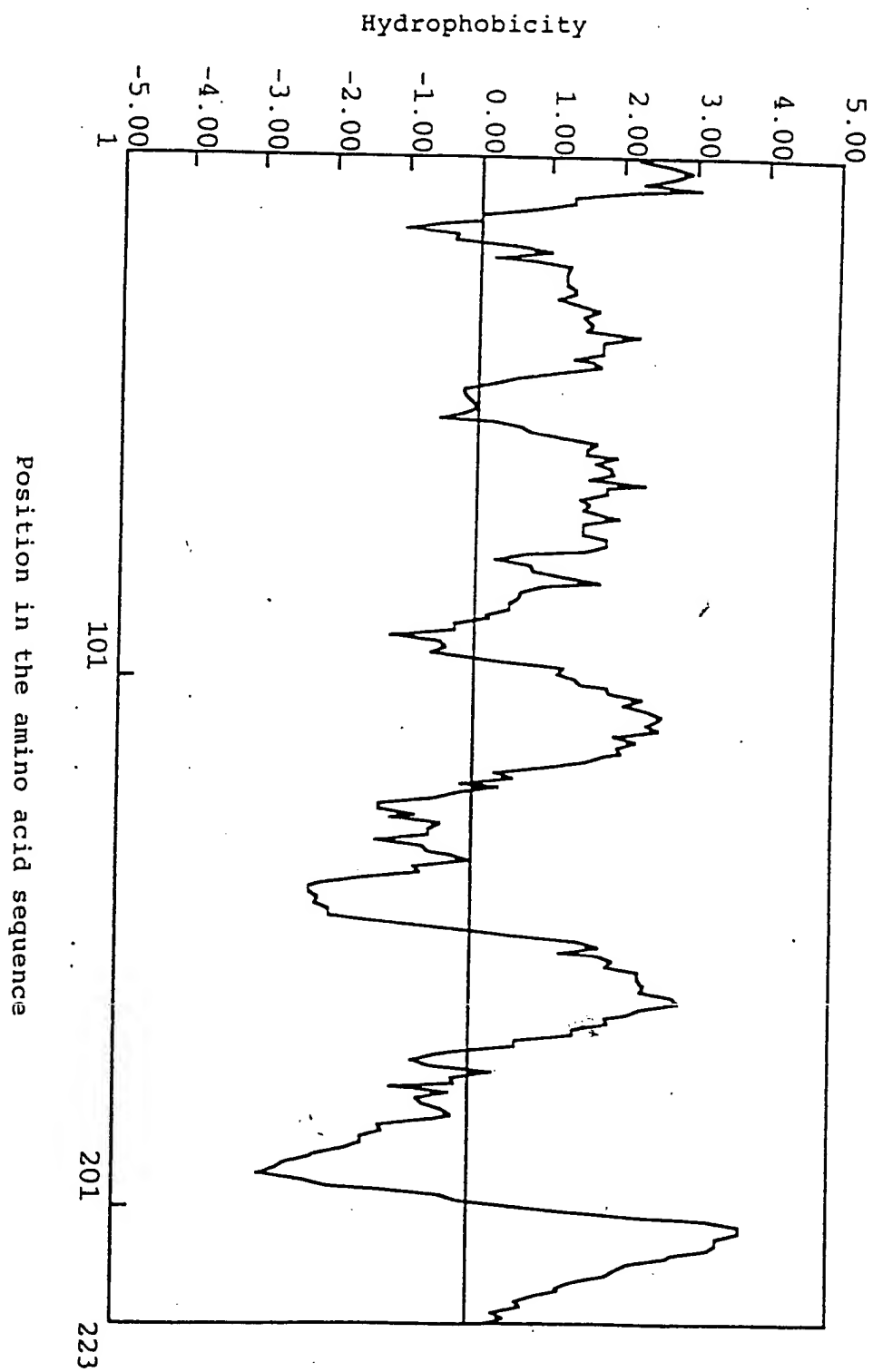
5'	GTG	GGC	ATG	GTG	GGC	AAC	ATC	CTG	CTG	GTG	CTG	GTG	ATC	GCC	CGG	GTG	CGC	CGG	54
	Val	Gly	Met	Val	Gly	Asn	Ile	Leu	Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	
	CTG	TAC	AAC	GTG	ACG	AAT	TTC	CTC	ATC	GGC	AAC	CTG	GCC	TTG	TCC	GAC	GTG	CTC	108
	Leu	Tyr	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	
	ATG	TGC	ACC	GCC	TGC	GTG	CCG	CTC	ACG	CTG	GCC	TAT	GCC	TTC	GAG	CCA	CGC	GGC	162
	Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	
	TGG	GTG	TTC	GGC	GGC	GGC	CTG	TGC	CAC	CTG	GTC	TTC	TTC	CTG	CAG	GCG	GTC	ACC	216
	Trp	Val	Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Ala	Val	Thr	
	GTC	TAT	GTG	TGC	GTG	TTC	ACG	CTC	ACC	ACC	ATC	GCA	GTG	GAC	CGC	TAC	GTC	GTG	270
	Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	
	CTG	GTG	CAC	CCG	CTG	AGG	CGG	CGC	ATC	TGC	CTG	CGC	CTC	AGC	GCC	TAC	GCT	GTG	324
	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	
	CTG	GCC	ATC	TGG	GTG	CTG	TCC	GCG	GTG	CTG	GCG	CTG	CCC	GCC	GCC	GTG	CAC	ACC	378
	Leu	Ala	Ile	Trp	Val	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	
	TAT	CAC	GTG	GAG	CTC	AAG	CCG	CAC	GAC	GTG	CGC	CTC	TGC	GAG	GAG	TTC	TGG	GGC	432
	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val	Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly	
	TCC	CAG	GAG	CGC	CAG	CGC	CAG	CTC	TAC	GCC	TGG	GGG	CTG	CTG	CTG	GTC	ACC	TAC	486
	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Val	Thr	Tyr	
	CTG	CTC	CCT	CTG	CTG	GTC	ATC	CTC	CTG	TCT	TAC	GCC	CGG	GTG	TCA	GTG	AAG	CTC	540
	Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr	Ala	Arg	Val	Ser	Val	Lys	Leu	
	CGC	AAC	CGC	GTG	GTG	CCG	GGC	CGC	GTG	ACC	CAG	AGC	CAG	GCC	GAC	TGG	GAC	CGC	594
	Arg	Asn	Arg	Val	Val	Pro	Gly	Arg	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	
	GCT	CGG	CGC	CGG	CGC	ACC	TTC	TGC	TTG	CTG	GTG	GTG	GTC	GTG	GTG	GTG	TTC	ACC	648
	Ala	Arg	Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	
	CTC	TGC	TGG	CTG	CCC	TTC	TTC	TTC	TTC	TTC	TTC	TTC	TTC	TTC	TTC	TTC	TTC	TTC	666
	Leu	Cys	Trp	Leu	Pro	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	

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Fig. 7

p19P2	1	VGWVGNI	10	LVTVARVR	20	NVTNELIGNL	30	ALSDVLEMTA	40	CVEPLTLAYAF	50
PG3-2/PG1-10	1	VGWVGNI	10	LVTVARVR	20	NVTNELIGNL	30	ALSDVLEMTA	40	CVEPLTLAYAF	50
p19P2	51	EPRCMVFE	60	LCHLVFE	70	VTVYVSVE	80	TTIAVD	90	LVHPLRRRI	100
PG3-2/PG1-10	51	EPRCMVFE	60	LCHLVFE	70	VTVYVSVE	80	TTIAVD	90	LVHPLRRRI	100
p19P2	101	---	110	---	120	---	130	---	140	---	150
PG3-2/PG1-10	101	LRLSAYAV	110	IWVLSAV	120	PAVHTYH	130	LKPHDVR	140	CE EFWGSQ	150
p19P2	151	---	160	TYLLP	170	LSYVRV	180	RNRV	190	QSQAD	200
PG3-2/PG1-10	151	QLYAW	160	TYLLP	170	LSYVRV	180	RNRV	190	QSQAD	200
p19P2	201	RRRTFC	210	WVVEAT	220	PYY	230	---	240	---	250
PG3-2/PG1-10	201	RRRTFC	210	WVVEAT	220	PYY	230	---	240	---	250

Fig. 8



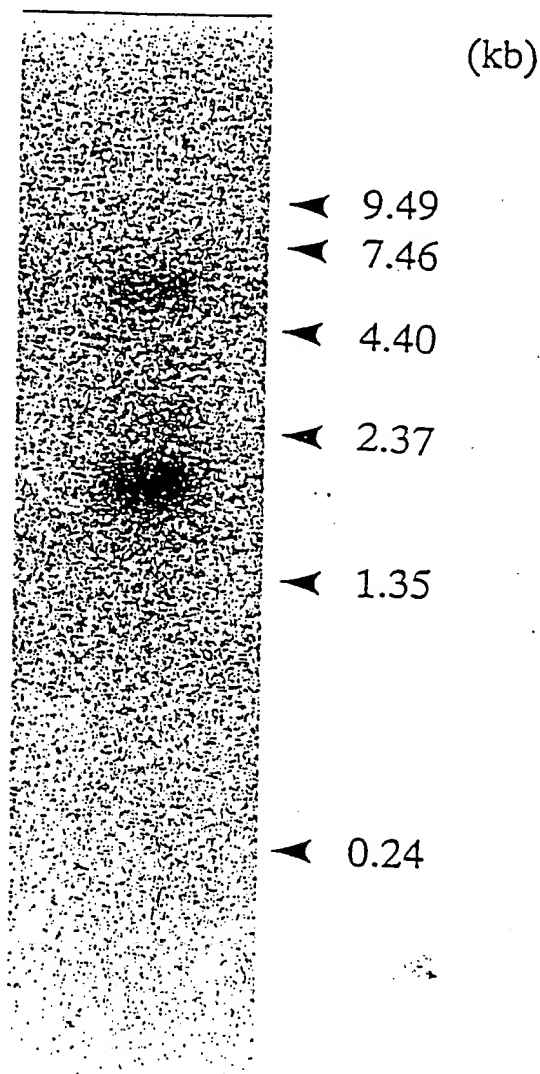
09576290 . 052300

Fig. 9

1	CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGGCCAGCAGAAATT	60
1		1
61	CTGCCCCCTTCTCCCGCGAGTGCTTCCCGCTCTCCAAACCCCACTCCCAGGTGGCCATG	120
1		Met 1
121	GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGGCTGCCGCCGGCG	180
1	AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla	21
181	GTCACAACCTCCCGCCAACAGAGCGCAGAGGCTCGGCGGGCAACGGGTGGTGGCTGGC	240
21	ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly	41
241	GCGGACGCTCCAGCCGTACGCCCTTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGGG	300
41	AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly	61
301	CTGATCGTGTCTCTACAGCGTCTGGTGGTCTGGTGGGCTGGTGGGCAACTGCCTGCTG	360
61	LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTGATCGCGCGGGTGGCGGGCTGCACAACGTGACGAACCTCCTCATCGGCAAC	420
81	ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTGTGCCAGCTGTCTCATGTGCACCGCTGCGTGGCGCTCAGCGTGGCCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTCGAGCCACGCGGCTGGGTGTTCGGCGGGCGCTGTGCCACCTGGTCTTCTTCTGTCAG	540
121	PheGluProArgGlyTrpValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTCACCGTCTATGTGTGGTGTTCACGCTCACCACCATCGCAGTGGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
601	GTGCTGGTGACCCGCTGAGGCGGCGCATCTCGCTGGCGCTCAGCGCTACGCTGTGCTG	660
161	ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
661	GCCATCTGGCGCTGTCCGCGGTGTGGCGCTGCCCGCGCGCTGCACACCTATCAGCTG	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGACGACGTGGCGCTCTGCGAGGAGTTCTGGGGCTCCAGGAGCGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCTGGGGCTGTGCTGGTACCTACCTGCTCCCTCTGCTGGTCATC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241
841	CTCCTGTCTTACGTCCGGGTGTGAGTGAAGCTCCGCAACCGCGTGGTGGCGGGCTGGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGGCGGACTGGGACCGCGCTCGGCGCGCGCGCACCTTCTGCTTGCTGGTG	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTCGTGGTGGTGTTCGCCGTCTGCTGGCTGCCGCTGCACGCTTCAACCTGCTGCGG	1020
281	ValValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCAAGCCATCGACCCTTACGCCCTTGGGCTGGTGCAGCTGCTCTGCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTCGCCATGAGTTCCGCCCTGTACAACCCCTTCATCTACGCTGGCTGCACGACAGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCGCGAGGAGCTGCGCAAACTGTTGGTTCGCTTGGCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAATATGACCGTCAGCGTGGTCACTCTGATGCCACTTAGCCAGGCCTTGGTCAAGGAGC	1260
361	GlnAsnMetThrValSerValValIle***	371
1261	TCCACTTCAACTGGCCTCTAGGGCACCCTCGAGGTCAATCTGGTGTCTATTCTCAGCA	1320
371		371
1321	CCAGAGCTAGC	1331
371		371

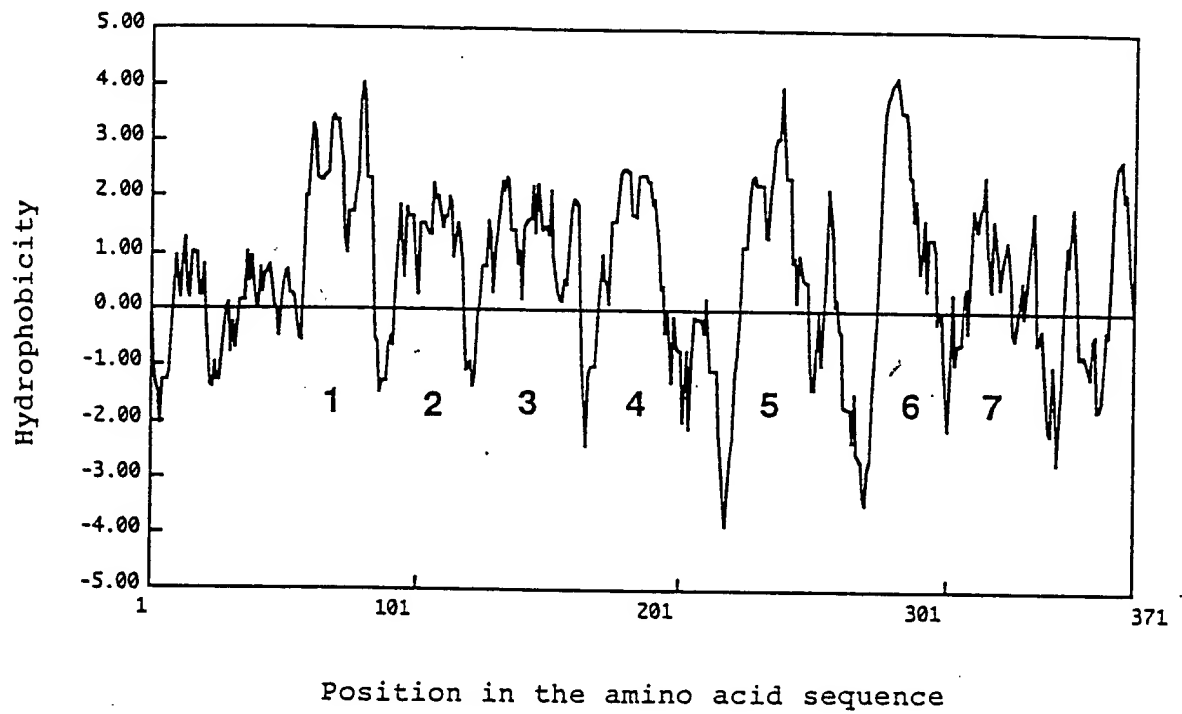
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Fig. 10



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Fig. 11



CT 3'

5		9			18			27		36		45		54				
	CTG	TGT	GTC	ATC	GCG	GTG	GAT	AGG	TAC	GTG	GTT	CTG	GTG	CAC	CCG	CTA	CGT	CGG
	Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg
		63				72			81			90		99				108
	CGC	ATT	TCA	CTG	AGG	CTC	AGC	GCC	TAC	GCG	GTG	CTG	GGC	ATC	TGG	GCT	CTA	TCT
	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser
		117				126			135			144		153				162
	GCA	GTG	CTG	GCG	CTG	CCG	GCC	GCG	GTG	CAC	ACC	TAC	CAT	GTG	GAG	CTC	AAG	CCC
	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro
		171				180			189			198		207				216
	CAC	GAC	GTG	AGC	CTC	TGC	GAG	GAG	TTC	TGG	GGC	TCG	CAG	GAG	CGC	CAA	CGC	CAG
	His	Asp	Val	Ser	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln
		225				234			243			252		261				270
	ATC	TAC	GCC	TGG	GGG	CTG	CTT	CTG	GGC	ACC	TAT	TTG	CTC	CCC	CTG	CTG	GCC	ATC
	Ile	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	Ile
		279				288			297			306		315				324
	CTC	CTG	TCT	TAC	GTA	CGG	GTG	TCA	GTG	AAG	CTG	AGG	AAC	CGC	GTG	GTG	CCT	GGC
	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly
		333				342			351			360		369				378
	AGC	GTG	ACC	CAG	AGT	CAA	GCT	GAC	TGG	GAC	CGA	GCG	CGT	CGC	CGC	CGC	ACT	TTC
	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe
		387				396			405			414		423				432
	TGT	CTG	CTG	GTG	GTG	GTG	GTG	GTA	GTG	TTC	ACG	CTC	TGC	TGG	CTG	CCC	TTC	TAC
	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Tyr

Fig. 13

p19P2
pg3-2/pg1-10
p5S38

1	VGMVGNVLIV	10	LVTARVRRLI	20	NVTNFIIGNL	30	ALSDVIMCTA	40	CVPLTLAYAF	50
1	VGMVGNILIV		LVTARVRRLI		NVTNFIIGNL		ALSDVIMCTA		CVPLTLAYAF	
-79	

50
50
50
-30

p19P2
pg3-2/pg1-10
p5S38

51	EPHGMVEGGG	60	LCHLVEFFLP	70	VTVYVSVEFTL	80	TTTAVDRIYV	90	LVHPLRRRI	100
51	EPHGMVEGGG		LCHLVEFFLP		VTVYVSVEFTL		TTTAVDRIYV		LVHPLRRRI	
-29	

100
100
21

p19P2
pg3-2/pg1-10
p5S38

101	LRLSAYAVLA	110	IMVLSAVLAL	120	PAVHTYHVE	130	LKPHDYRLCE	140	EFWGSQEROR	150
101	LRLSAYAVLA		IMVLSAVLAL		PAVHTYHVE		LKPHDYRLCE		EFWGSQEROR	
22	LRLSAYAVLS		IMVLSAVLAL		PAVHTYHVE		LKPHDYRLCE		EFWGSQEROR	

150
150
71

p19P2
pg3-2/pg1-10
p5S38

151	GLLIV	160	TYLLPLLVIT	170	LSYVRVSVKL	180	RNRVVPGLVT	190	QSQADWDRAR	200
151	GLLIV		TYLLPLLVIT		LSYVRVSVKL		RNRVVPGLVT		QSQADWDRAR	
72	QTYAMGILLG		TYLLPLLVIT		LSYVRVSVKL		RNRVVPGLVT		QSQADWDRAR	

200
200
121

p19P2
pg3-2/pg1-10
p5S38

201	RRRTFCLLV	210	VVVFALCWL	220	PFY	230	240	250
201	RRRTFCLLV		VVVFALCWL		PFY		
122	RRRTFCLLV		VVVFALCWL		PFY		

250
250
171

Fig. 14

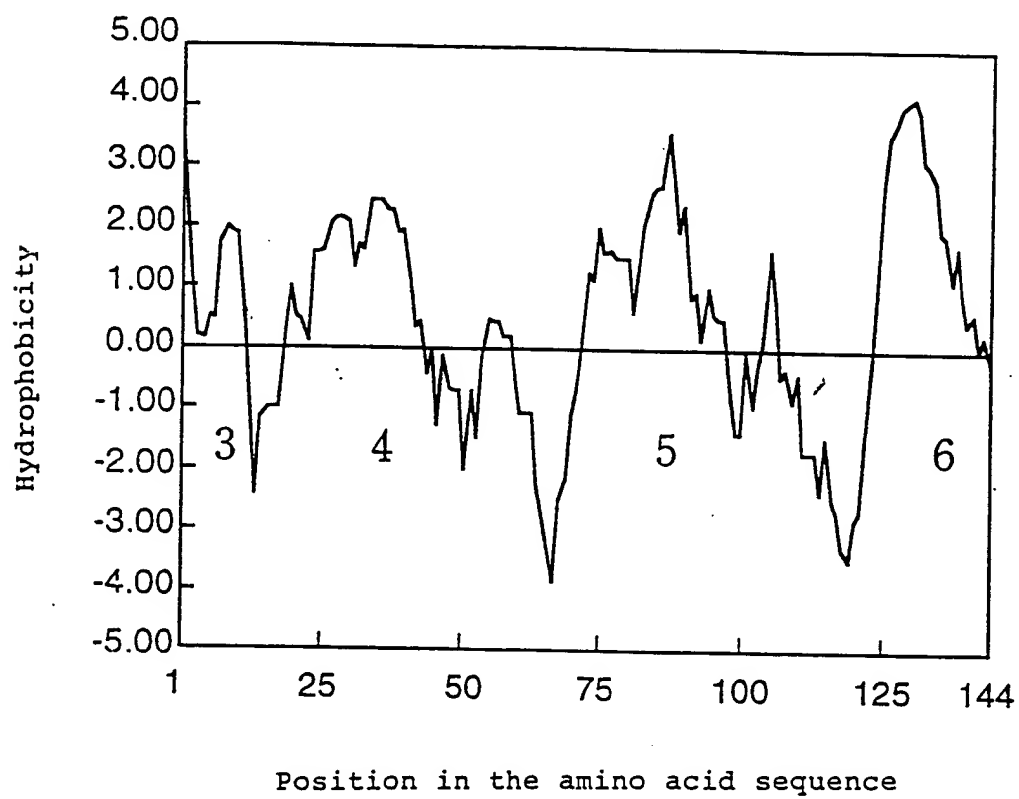
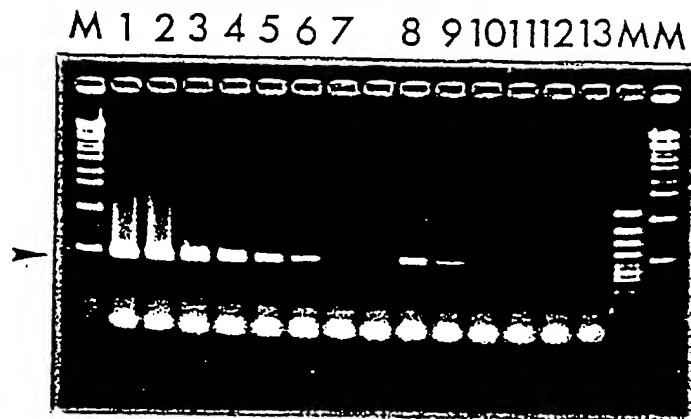
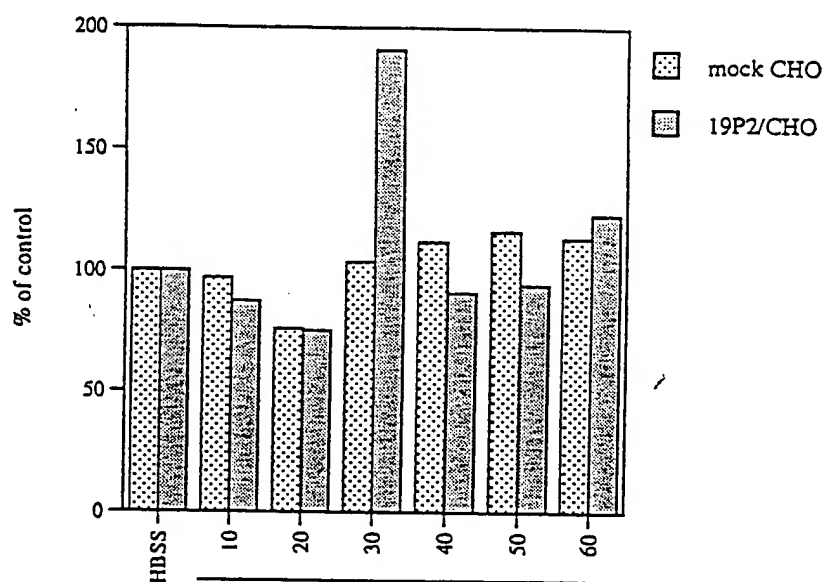


Fig. 15



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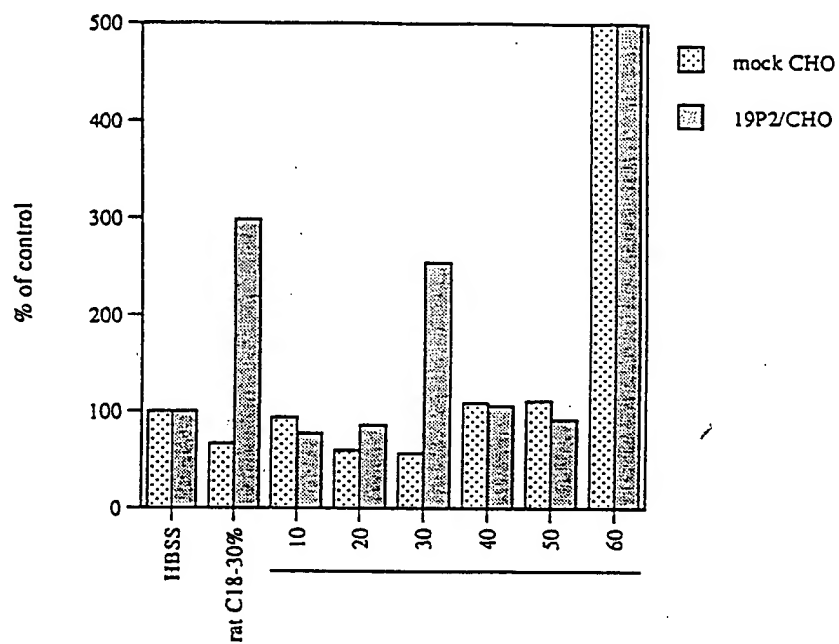
Fig. 16



rat whole brain extract

C₁₈-column CH₃CN elution (%)

Fig. 17



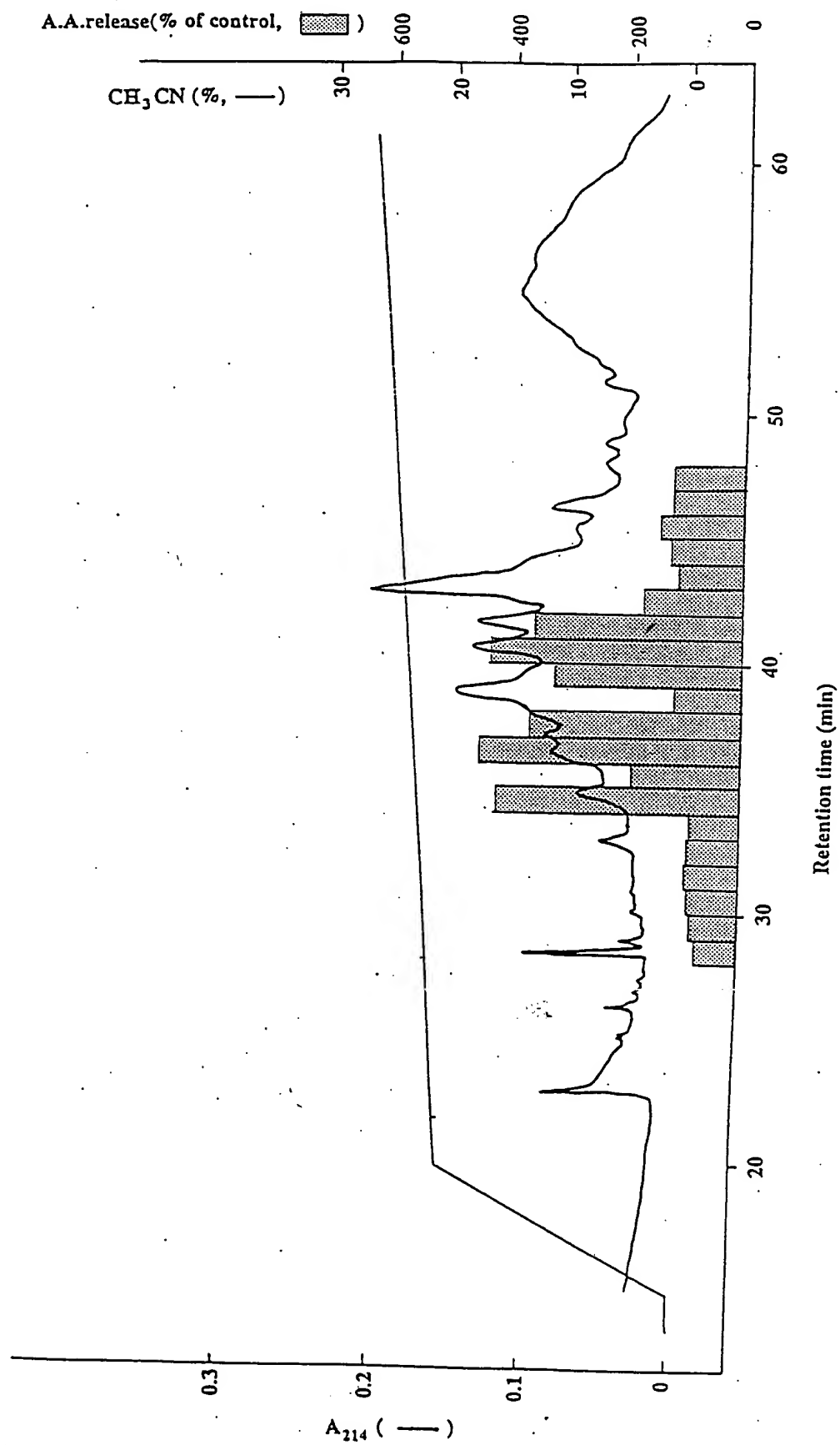
bovine hypothalamus extract

C₁₈-column CH₃CN elution (%)

000000 000000

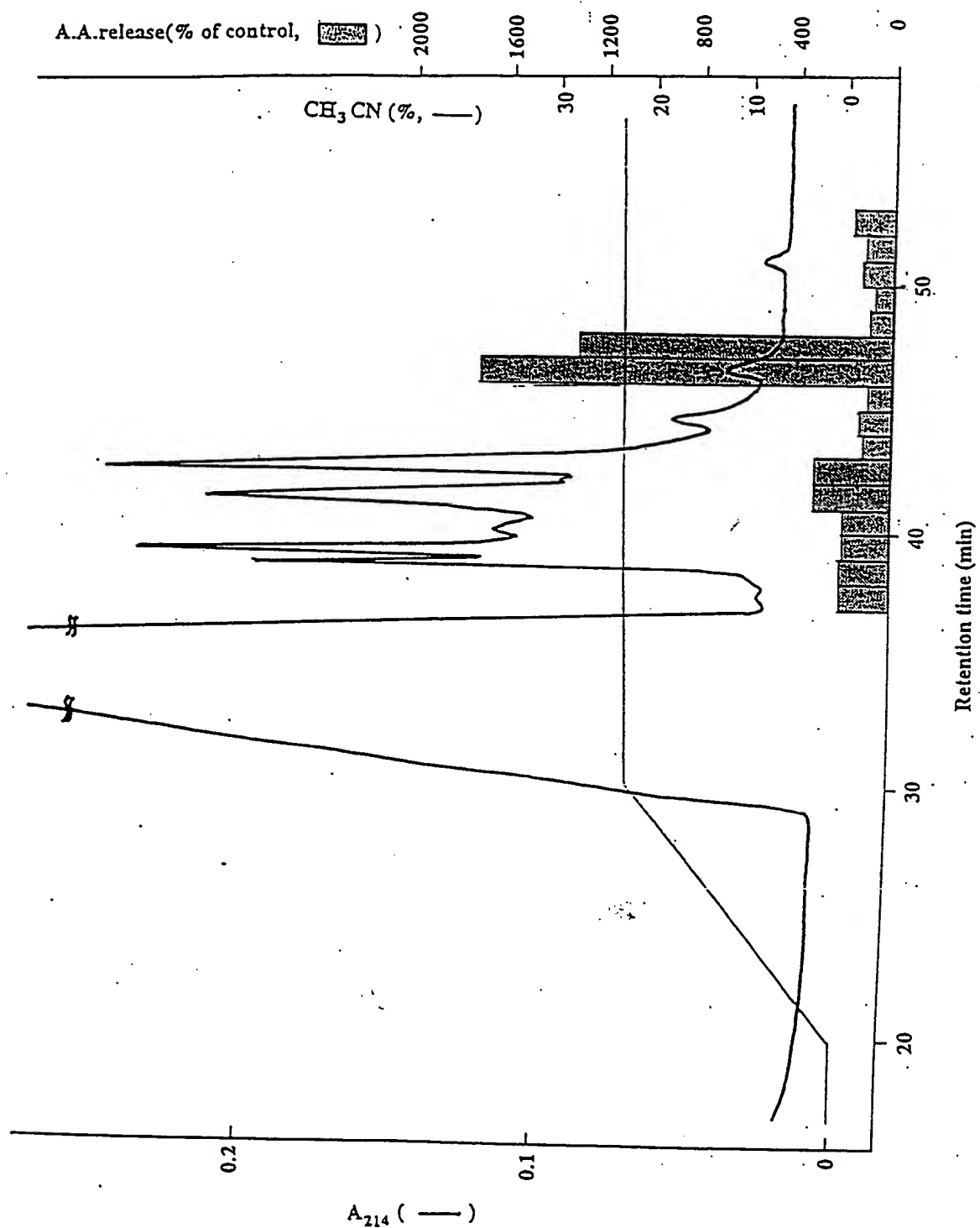
18/53

Fig. 1



19/53

Fig. 19



006250" 06292560

Fig. 20

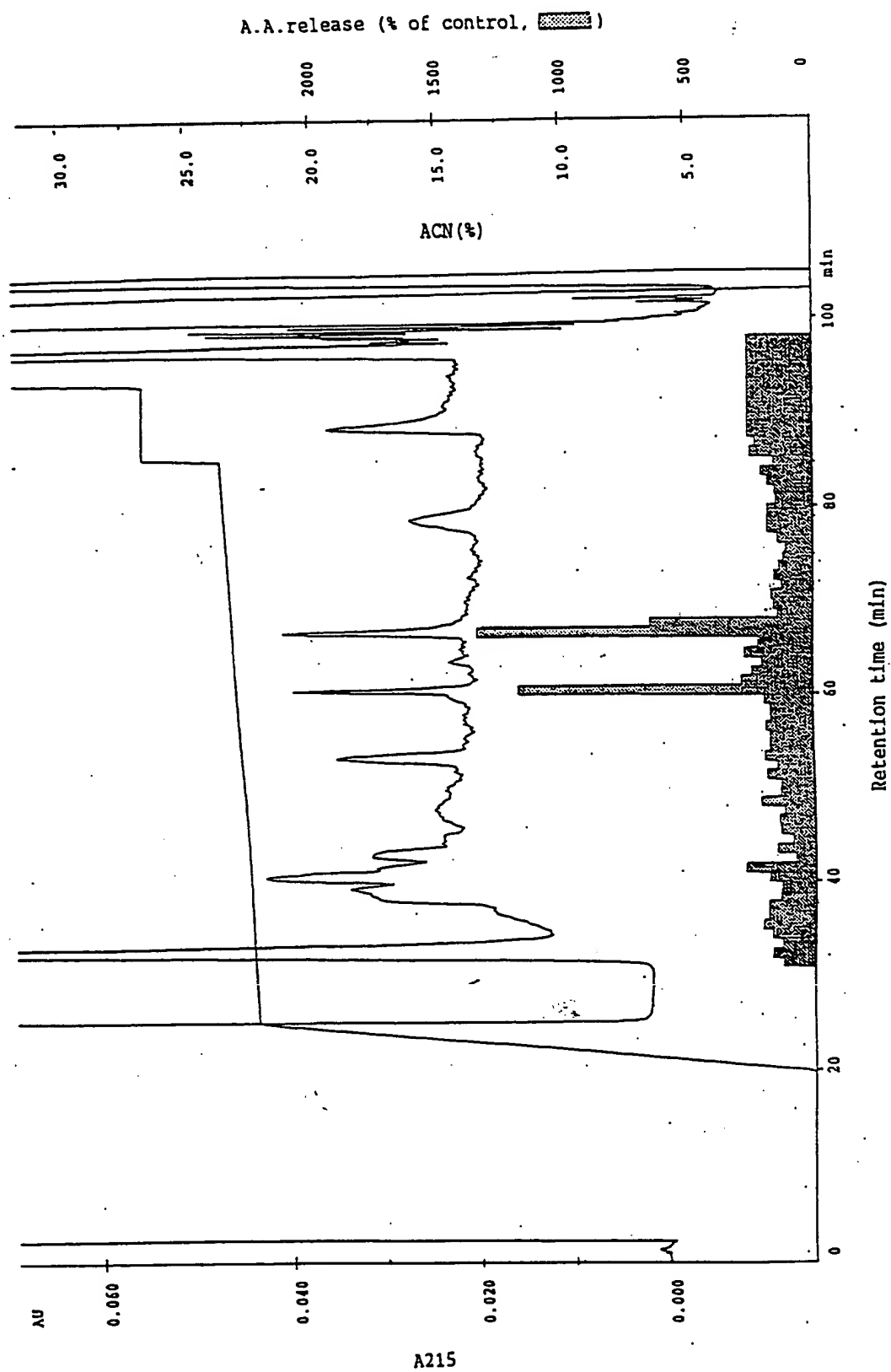
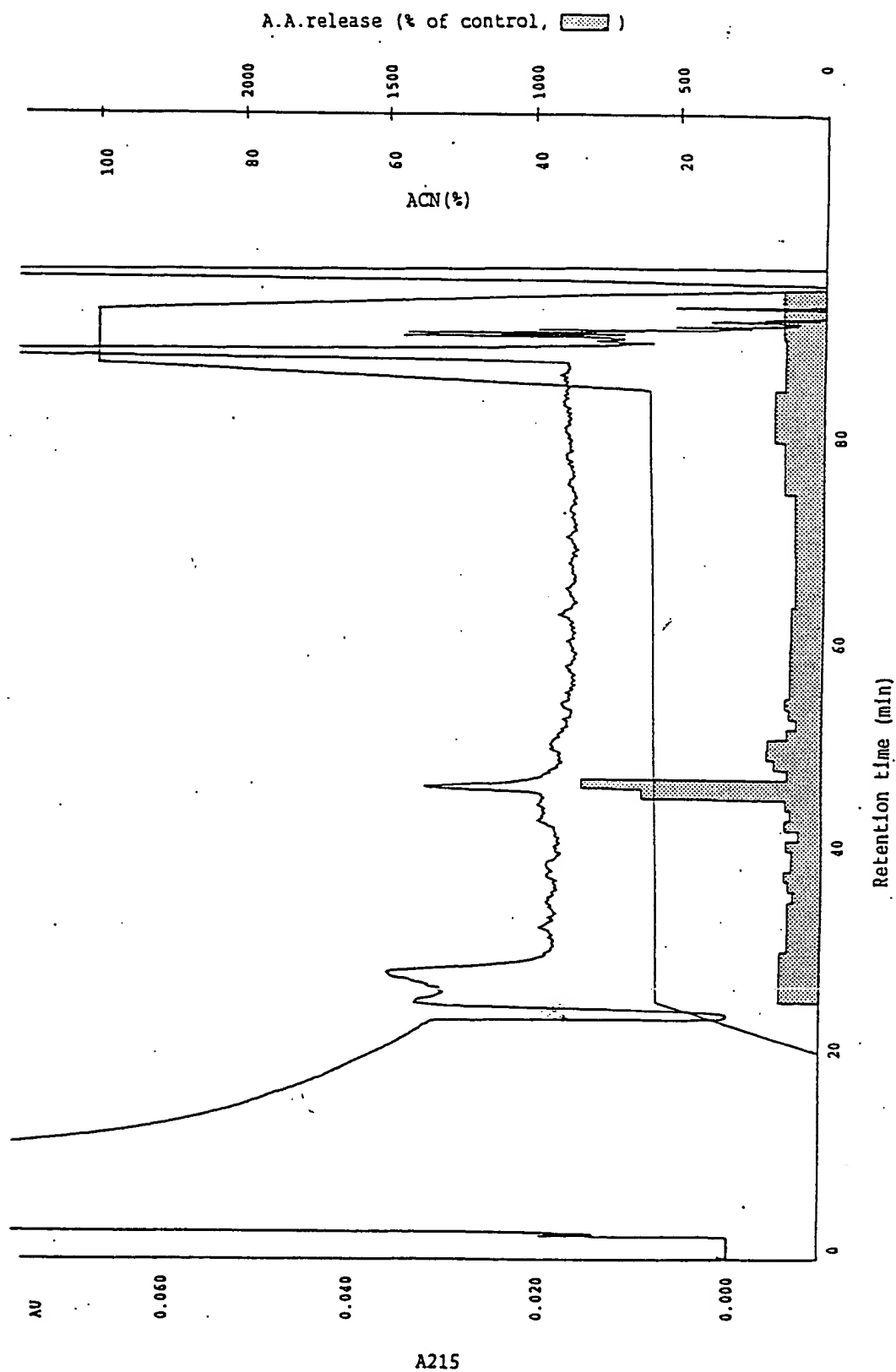


Fig. 21




```

      P5-1
      9          18          27          36          45          54
5'  GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr
                                     63          72
    GCG GGC CGT GGG ATC CGG CCC G 3'
    --- --- --- --- --- --- ---
    Ala Gly Arg Gly Ile Arg Pro
      P3-2

```

Fig. 23

1	GTGGAATGAAGGCGGTGGGGCCTGGCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
	 PDN	
120	CCTGCCT	126
39	<u>ProAla</u>	40

006250" 0529/660

Fig. 24(a)

1	GTGGAATGAAGCGGTGGGGGCTGGCTCCTCTGCCTGCTGCTGCTGGGCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
120	CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCGTGGGCTGCTTCGGCCGGCGAAGAGCT	179
39	ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgAla	58
180	CCCCCGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCTGGAA	239
59	AlaProGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu	78
240	GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGCGGCTGACGGCCCAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAACAGCGGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT	359
98		98
360	AATAAAAGCAGCTGGCTTGTT	380
98		98

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Fig. 24(b)

1	GTGGAATGAAGGCGGTGGGGGCCTGGCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
120	CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCGTGGGCCGCTTCGGCCGGCGAAGAGCT	179
39	ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla	58
180	GCCCTGGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCTGGAA	239
59	AlaLeuGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu	78
240	GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGCGGCTGACGGCCAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAACAGCGGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT	359
98		98
360	AATAAAAGCAGCTGGCTTGTT	380
98		98

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Fig. 25

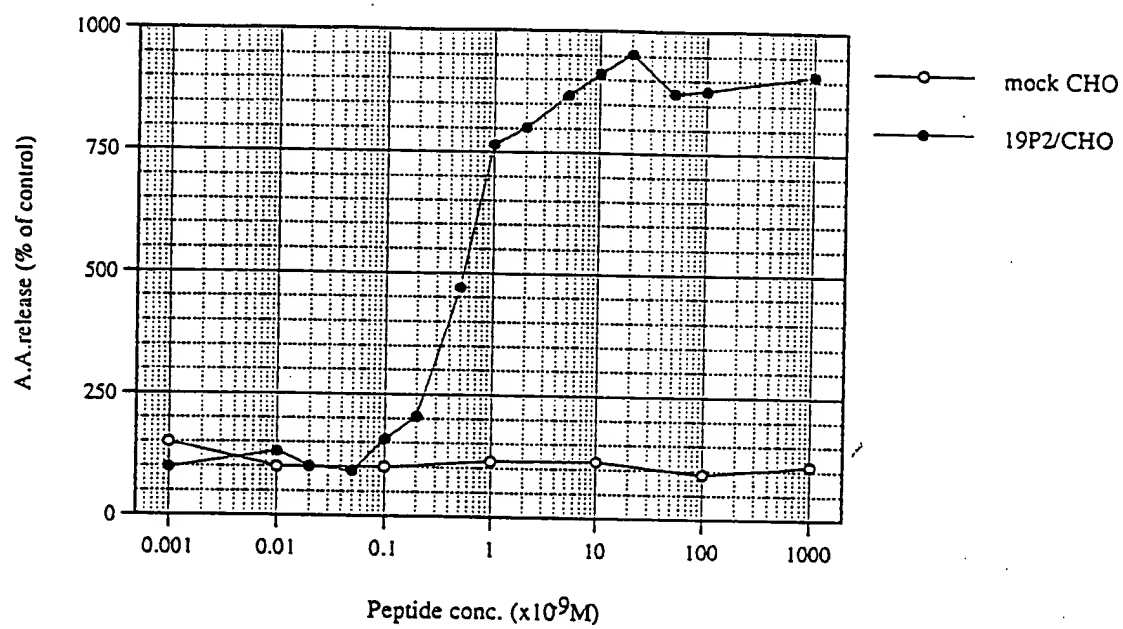
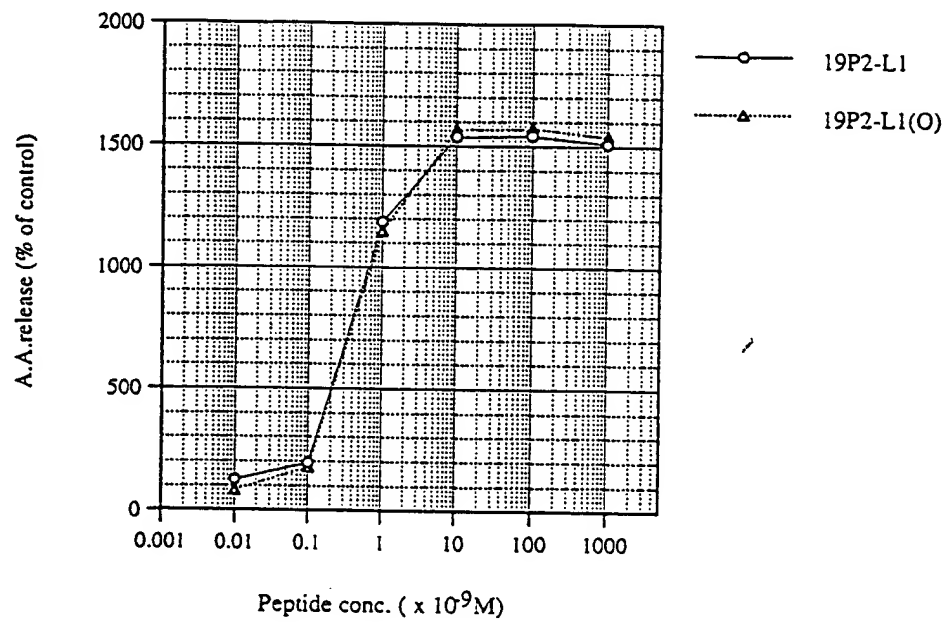
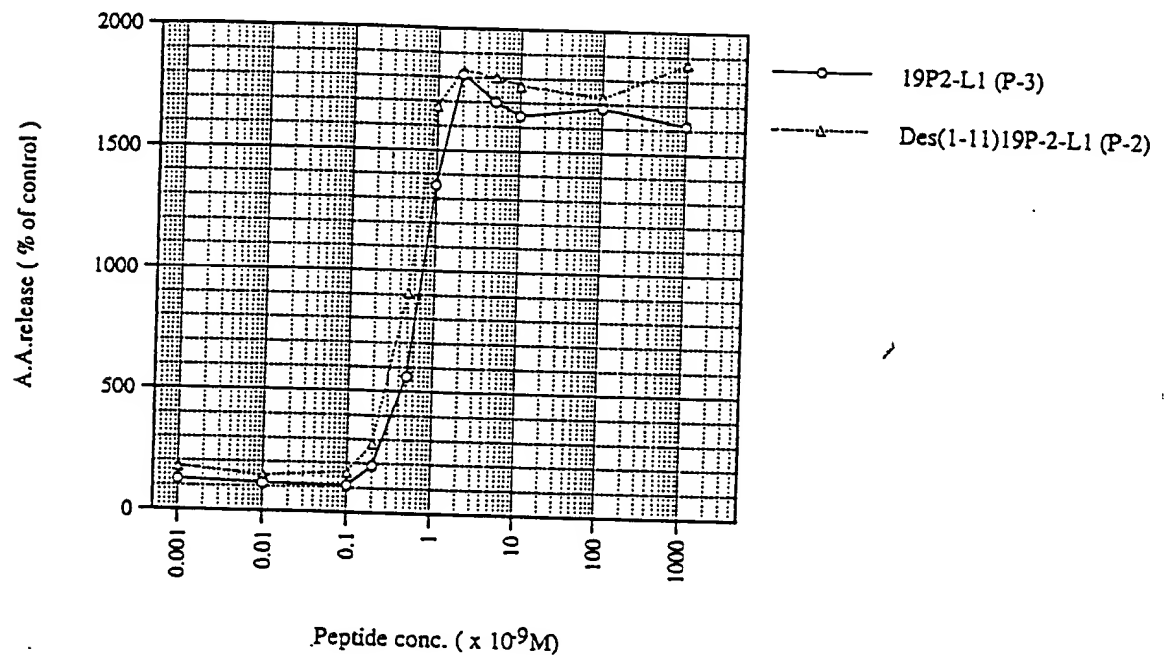


Fig. 26



003250-0629/550

Fig. 27



10	20	30	40	50	60
ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG
70	80	90	100	110	120
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCGCC
130	140	150	160	170	180
CTGCCCCCAG	GGGTACAGG	GGGGGCCTGG	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA
190	200	210	220	230	240
GCATCCTGGG	GTGGGGTTT	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCGGA
250	260	270	280	290	300
CAGGTGCTCC	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACTCCTC	ACCACACGGG
310	320	330	340	350	360
TGGCCTGGGG	CTGAGTGAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG
370	380	390	400	410	420
GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA
430	440	450	460	470	480
ATGGGCGCTC	CGGGTGAACC	TCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA
490	500	510	520	530	540
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC
550	560	570	580	590	600
AGGCCTCCAT	GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCTG	CCTGGTACGC
610	620	630	640	650	660
AGGCCGTGGG	ATCCGGCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG
670	680	690	700	710	720
ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC
730	740	750	760	770	780
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA.

Fig. 30

genome	10	20	30	40	50	
cDNA	1 ATGAAGGCGG	TGGGGGCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	50
	1 ATGAAGGCGG	TGGGGGCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	50
genome	60	70	80	90	100	
cDNA	51 CCTGCAGGGG	GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	100
	51 CCTGCAGGGG	GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	100
genome	110	120	130	140	150	
cDNA	101 GTGAGTGTCT	AGCCCCGCCC	CTGCCCCCAG	GGGTACAGG	GGGGGCTGG	150
	101 -----	-----	-----	-----	-----	150
genome	160	170	180	190	200	
cDNA	151 CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA	GCATCCTGGG	GTTGGGGTTT	200
	151 -----	-----	-----	-----	-----	200
genome	210	220	230	240	250	
cDNA	201 GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCCGA	CAGGTGCTCC	250
	201 -----	-----	-----	-----	-----	250
genome	260	270	280	290	300	
cDNA	251 CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACCTCTC	ACCACACGGG	300
	251 -----	-----	-----	-----	-----	300
genome	310	320	330	340	350	
cDNA	301 TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	350
	301 -----	-----	-----	-----	-----	350
genome	360	370	380	390	400	
cDNA	351 GGAAAGGAAG	GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	400
	351 -----	-----	-----	-----	-----	400
genome	410	420	430	440	450	
cDNA	401 AAGCCACCCC	AGCACCAGAA	ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	450
	401 -----	-----	-----	-----	-----	450
genome	460	470	480	490	500	
cDNA	451 GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA	GGCAGCCATG	AGCTGAGCAC	500
	451 -----	-----	-----	-----	-----	500
genome	510	520	530	540	550	
cDNA	501 ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	AGGCCTCCAT	550
	501 -----	-----	-----	-----	-----	550
genome	560	570	580	590	600	
cDNA	551 GCGCTCTTCT	CTCTCTTTTC	AGCCCCCGAC	ATCAACCCCTG	CCTGGTACGC	600
	551 -----	-----	-----	-----	-----	600
genome	610	620	630	640	650	
cDNA	601 AGGCCGTGGG	ATCCGGCCCG	TGGGCGGCTT	CGGCCGGCGA	AGAGCTGCCC	650
	601 GGGCCGTGGG	ATCCGGCCCG	TGGGCGGCTT	CGGCCGGCGA	AGAGCTGCCC	650
genome	660	670	680	690	700	
cDNA	651 TGGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	700
	651 CGGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	700
genome	710	720	730	740	750	
cDNA	701 CTGGAAGGCG	GTGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	750
	701 CTGGAAGGCG	GTGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	750
genome	760	770	780	790	800	
cDNA	751 CCAGCTGGTC	CAGGAATAA.	800
	751 CCAGCTGGTC	CAGGAATAA.	800

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Fig. 31

5'	ATG	AAG	⁹ GCG	GTG	GGG	¹⁸ GCC	TGG	CTC	²⁷ CTC	TGC	CTG	³⁶ CTG	CTG	CTG	⁴⁵ GGC	CTG	GCC	⁵⁴ CTG
	M	K	A	V	G	A	W	L	L	C	L	L	L	L	G	L	A	L
	CAG	GGG	⁶³ GCT	GCC	AGC	⁷² AGA	GCC	CAC	⁸¹ CAG	CAC	TCC	⁹⁰ ATG	GAG	ATC	⁹⁹ CGC	ACC	CCC	¹⁰⁸ GAC
	Q	G	A	A	S	R	A	H	Q	H	S	M	E	I	R	T	P	D
	ATC	AAC	¹¹⁷ CCT	GCC	TGG	¹²⁶ TAC	GCA	GGC	¹³⁵ CGT	GGG	ATC	¹⁴⁴ CGG	CCC	GTG	¹⁵³ GGC	CGC	TTC	¹⁶² GGC
	I	N	P	A	W	Y	A	G	R	G	I	R	P	V	G	R	F	G
	CGG	CGA	¹⁷¹ AGA	GCT	GCC	¹⁸⁰ CTG	GGG	GAC	¹⁸⁹ GGA	CCC	AGG	¹⁹⁸ CCT	GGC	CCC	²⁰⁷ CGG	CGT	GTG	²¹⁶ CCG
	R	R	R	A	A	L	G	D	G	P	R	P	G	P	R	R	V	P
	GCC	TGC	²²⁵ TTC	CGC	CTG	²³⁴ GAA	GGC	GGT	²⁴³ GCT	GAG	CCC	²⁵² TCC	CGA	GCC	²⁶¹ CTC	CCG	GGG	²⁷⁰ CGG
	A	C	F	R	L	E	G	G	A	E	P	S	R	A	L	P	G	R
	CTG	ACG	²⁷⁹ GCC	CAG	CTG	²⁸⁸ GTC	CAG	GAA	²⁹⁷ TAA	3'								
	L	T	A	Q	L	V	Q	E	*									

003250-05292550

Fig. 32

1	GGCATCATCCAGGAAGACGGAGCATGGCCCTGAAGACGTGGCTTCTGTGCTTGCTGCTG	59
1	MetAlaLeuLysThrTrpLeuLeuCysLeuLeuLeu	12
60	CTAAGCTTGGTCCTCCCAGGGGCTTCCAGCCGAGCCCACCAGCACTCCATGGAGACAAGA	119
13	LeuSerLeuValLeuProGlyAlaSerSerArgAlaHisGlnHisSerMetGluThrArg	32
120	ACCCCTGATATCAATCCTGCCTGGTACACGGGCCGCGGGATCAGGCCTGTGGGCCGCTTC	179
33	ThrProAspIleAsnProAlaTrpTyrThrGlyArgGlyIleArgProValGlyArgPhe	52
180	GGCAGGAGAAGGGCAACCCCCAGGGATGTCACTGGACTTGGCCAACTCAGCTGCCTCCCA	239
53	GlyArgArgArgAlaThrProArgAspValThrGlyLeuGlyGlnLeuSerCysLeuPro	72
240	CTGGATGGACGCACCAAGTTCTCTCAGCGTGGATAACACCCCAGCTCGAGAAGACAGTGC	299
73	LeuAspGlyArgThrLysPheSerGlnArgGly***	83
300	TGCTGAGCCCCAAGCCCACACTCCCTGTCCCCTGCAGACCCTCCTCTACCCTCCCTCTCCT	359
83		83
360	CTGCT	364
83		83

bovine.aa				M K A V G A W L L		
		10	20	30	40	50
bovine.seq	-18GT	GGAATGAAGG	CGGTGGGGGC	CTGGCTCCTC	
rat.seq	1 GGCATCATCC	AGGAAGACGG	AGCATG---G	CCCTGAAGAC	<u>GTGGCTTCTG</u>	32 50
bovine.aa		C L L L L G L A L Q	G A A S R A H			
		60	70	80	90	100
bovine.seq	33 TGCTTGCTGC	TGCTGGGGCT	GGCCCTGCAG	GGGGCTGCCA	GCAGAGCCCCA	
rat.seq	51 <u>TGCTTGCTGC</u>	<u>TGCTAAGCTT</u>	<u>GTCCTCCCA</u>	<u>GGGGCTTCCA</u>	<u>GCAGAGCCCCA</u>	82 100
		R1				
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		110	120	130	140	150
bovine.seq	83 CCAGCACTCC	ATGGAGATCC	GCACCCCGCA	CATCAACCCT	GCCTGGTAGC	
rat.seq	101 CCAGCACTCC	ATGGAGACAA	GAACCCCTGA	TATCAATCCT	<u>GCCTGGTACA</u>	132 150
					R3	
bovine.aa		G R G I R P V G R F	G R R R A A			
		160	170	180	190	200
bovine.seq	133 CGGGCCGTGG	GATCCGGCCC	GTGGGCCCGT	TCGGCCCGGG	AAGAGCTGCC	
rat.seq	151 <u>CGGGCCGCGG</u>	<u>GATCAGGCCT</u>	<u>GTGGGCCCGT</u>	<u>TCGGCAGGAG</u>	<u>AAGGGCAACC</u>	182 200
			R4			
bovine.aa		P G D G P R P G P R	R V P A C F R			
		210	220	230	240	250
bovine.seq	183 CCGGGGGAGC	GACCCAGGCC	TGGCCCCCGG	CGTGTGCOGG	CCTGCTTCCG	
rat.seq	201 CCGAGGGATG	TCACTGGACT	TGGC-----	---CAACTCA	GCTGCCTCCC	232 250
bovine.aa		L E G G A E P S R A	L P G R L T A			
		260	270	280	290	300
bovine.seq	233 CCTGGAAGGC	GGCGTGAGC	CCTCCCGAGC	CCTCCCCGGG	CGGCTGACGG	
rat.seq	251 ACTGGATGGA	CGCACCAAGT	TCTCTCAGCG	TGGATAACAC	CCCAGCTCGA	282 300
bovine.aa		Q L V Q E *				
		310	320	330	340	350
bovine.seq	283 CCCAGCTGGT	CCAGGAATAA	CAGCGGGAGC	CTGCCCCCCA	CCCTCCTCC	
rat.seq	301 GAAGACAGTG	CTGCTGAGCC	CAAGCCCACA	CTCCCTGTCC	CCTGCAGACC	332 350
bovine.aa						
		360	370	380	390	400
bovine.seq	333 TCCACCAGCC	ACCTTCCCTC	CAGTCCTAAT	AAAAGCAGCT	GGCTTGTT..	
rat.seq	351 CTCTCTTACC	CTCCCTCTCC	TCTGCT....	382 400

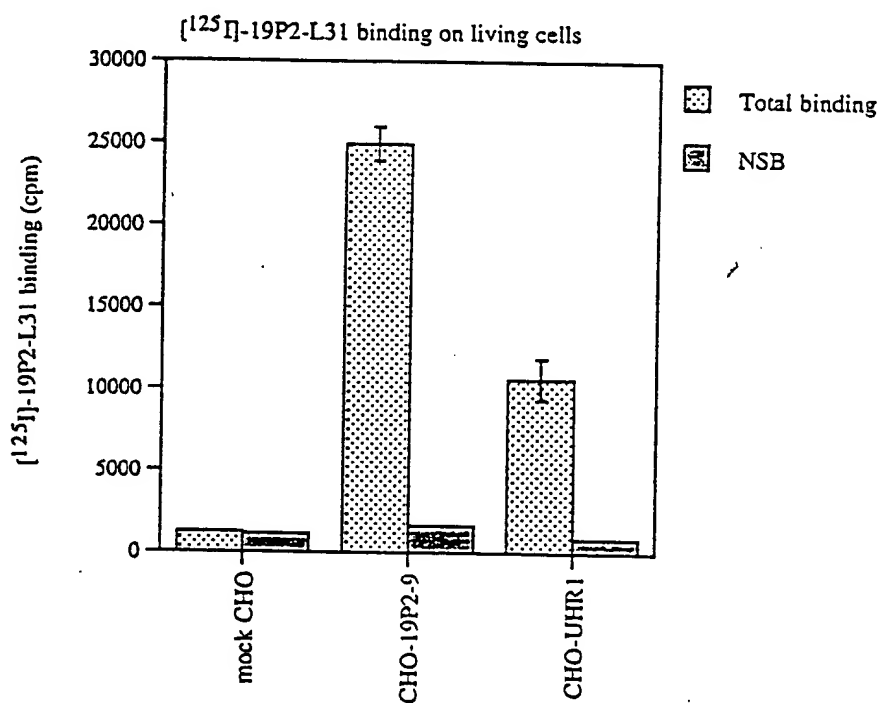
Fig. 34

1	GGCCTCCTCGGAGGAGCCAAGGGATGAAGGTGCTGAGGGCCTGGCTCCTGTGCCTGCTG	59
1	MetLysValLeuArgAlaTrpLeuLeuCysLeuLeu	12
60	ATGCTGGGCCTGGCCCTGCGGGGAGCTGCAAGTCGTACCCATCGGCACTCCATGGAGATC	119
13	MetLeuGlyLeuAlaLeuArgGlyAlaAlaSerArgThrHisArgHisSerMetGluIle	32
120	CGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGATCAGGCCTGTGGGCGCG	179
33	ArgThrProAspIleAsnProAlaTrpTyrAlaSerArgGlyIleArgProValGlyArg	52
180	TTCGGTCGGAGGAGGGCAACCCTGGGGGACGTCCCCAAGCCTGGCCTGCGACCCCGGCTG	239
53	PheGlyArgArgArgAlaThrLeuGlyAspValProLysProGlyLeuArgProArgLeu	72
240	ACCTGCTTCCCCCTGGAAGGCGGTGCTATGTCGTCCCAGGATGGCTGACAGCCAGCTTGT	299
73	ThrCysPheProLeuGluGlyGlyAlaMetSerSerGlnAspGly***	87
300	CAAGAACTCACTCTGGAGCCTCCCCACCCACCCCTCTCCTCTCCTTCGGGCTCCTTTC	359
87		87
360	CC	361
87		87

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		10	20	30	40	50	
bovine.aa	1	MEAVGAWLLC	LLLLGLALQG	AASRAHQHSM	EIRTPDINPA	WYAGRGIRFV	50
rat.aa	1	M-ALKTWLLC	LLLLSVLPG	ASSRAHQHSM	ETRTPDINPA	WYTGRGIRFV	50
human.aa	1	MKVLRAWLLC	LLMLGLALRG	AASRTHRHSM	EIRTPDINPA	WYASRGIRFV	50
		60	70	80	90	100	
bovine.aa	51	GRFGRRRAAP	GDGPRPGPRR	VPACFRLEGG	AEPSRALPGR	LTAQLVQE*	100
rat.aa	51	GRFGRRRATP	RDVTGLG---	QLSCLPLDGR	TKFSQSG*..	100
human.aa	51	GRFGRRRATL	GDVFKGLRPP	RLTCFPLEGG	AMSSQDS*..	100

Fig. 36



cells; 0.5×10^7 cells/ml

[¹²⁵I]-19P2-L31; 200pM (avg. 63857.3cpm)

NSB; 200nM (x 1,000)

reaction; RT, 2.5hr

in HBSS + 0.05% BSA + 0.05% CHAPS
in 100 μ l

Fig. 37

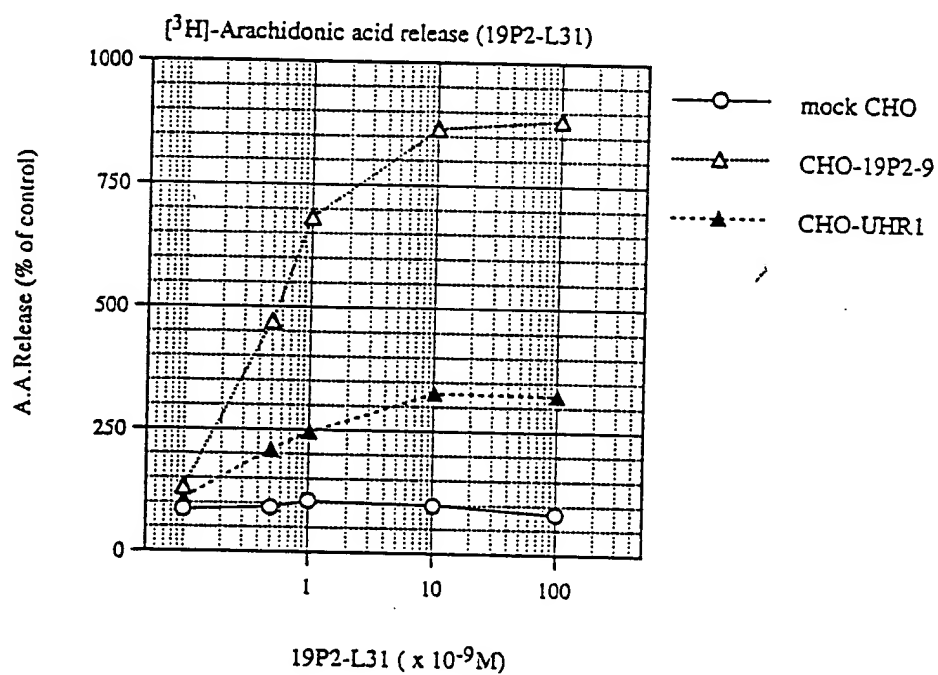
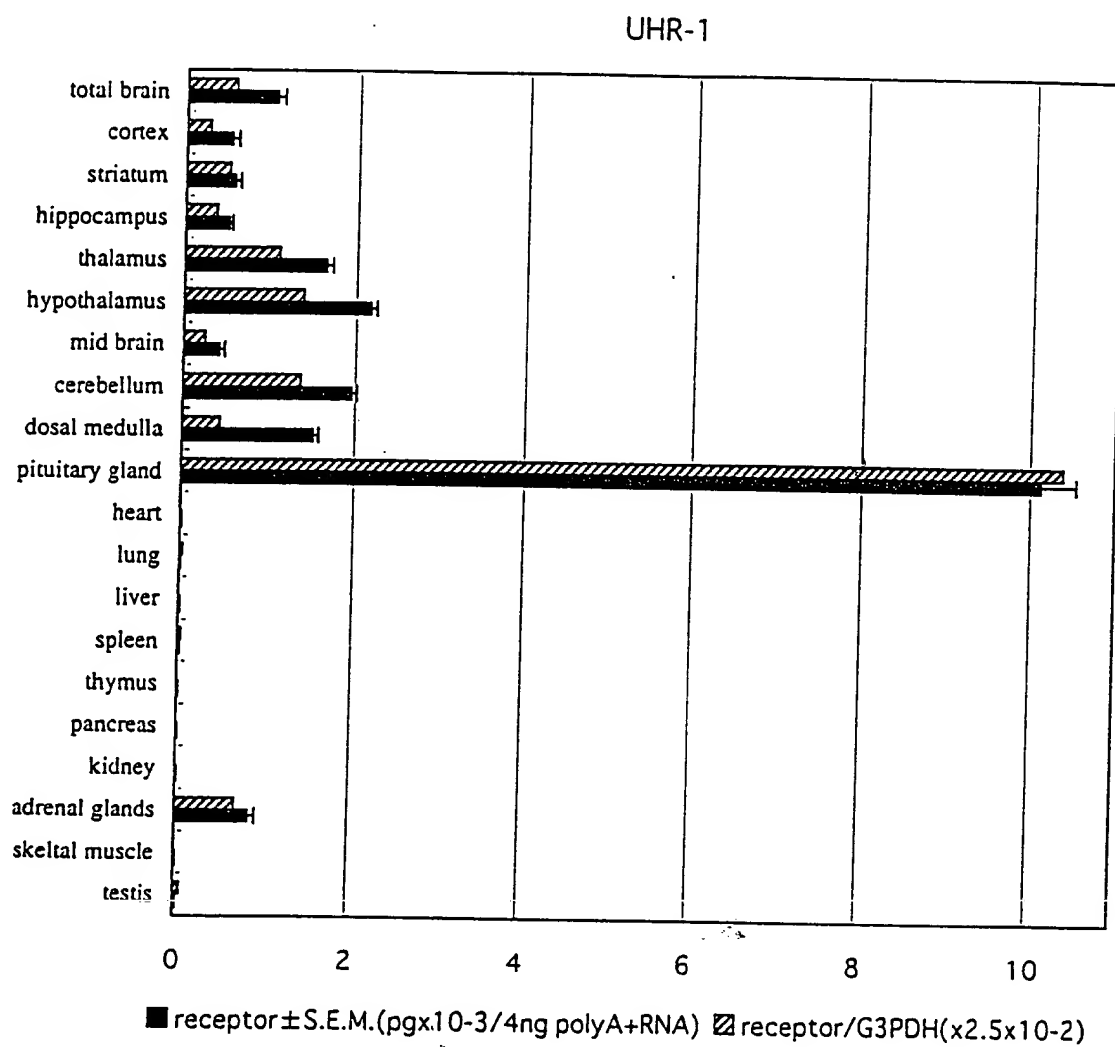


Fig. 38



006350"0629/660

Fig. 39

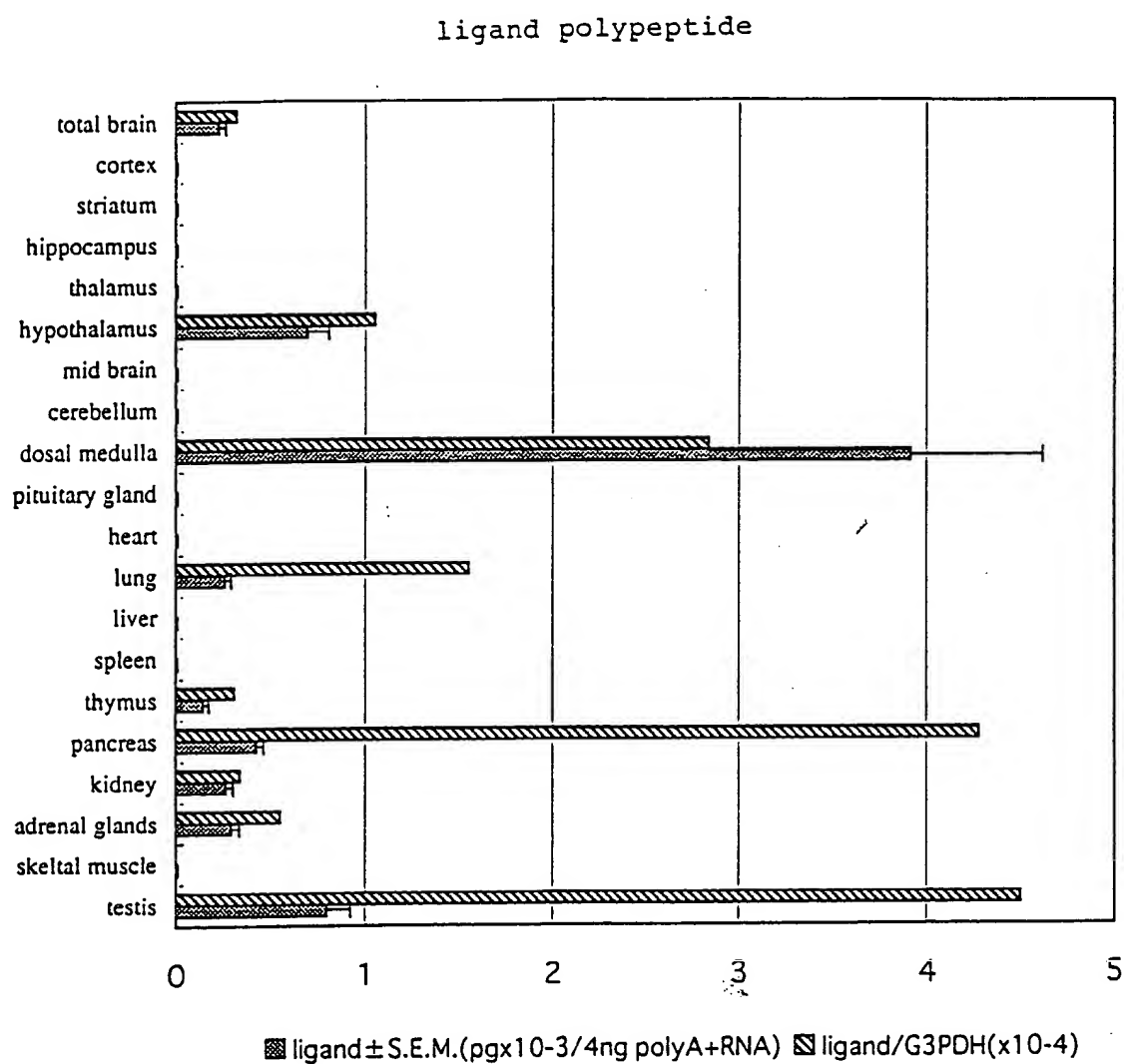


Fig. 40

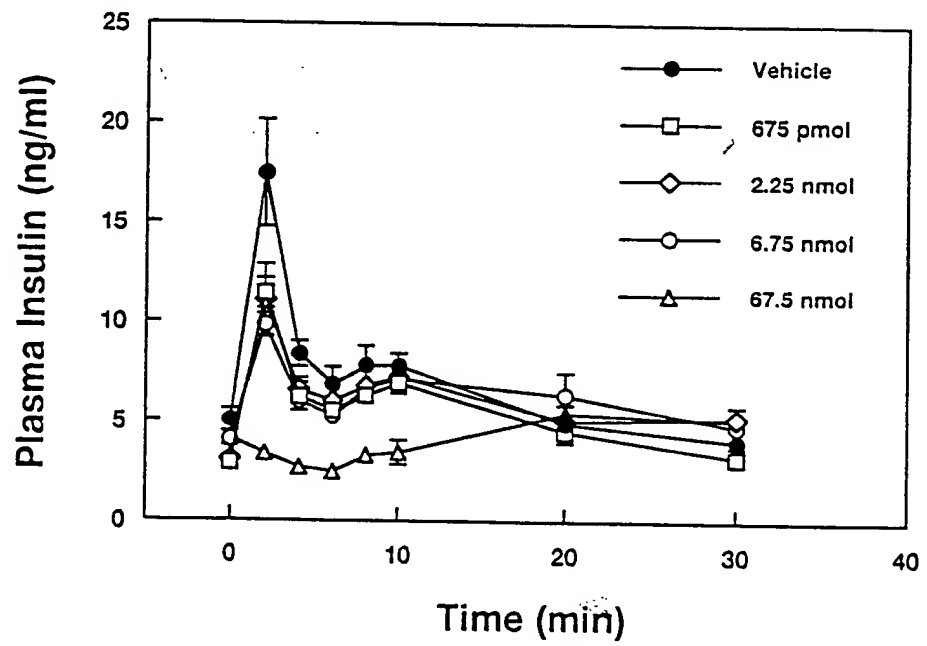
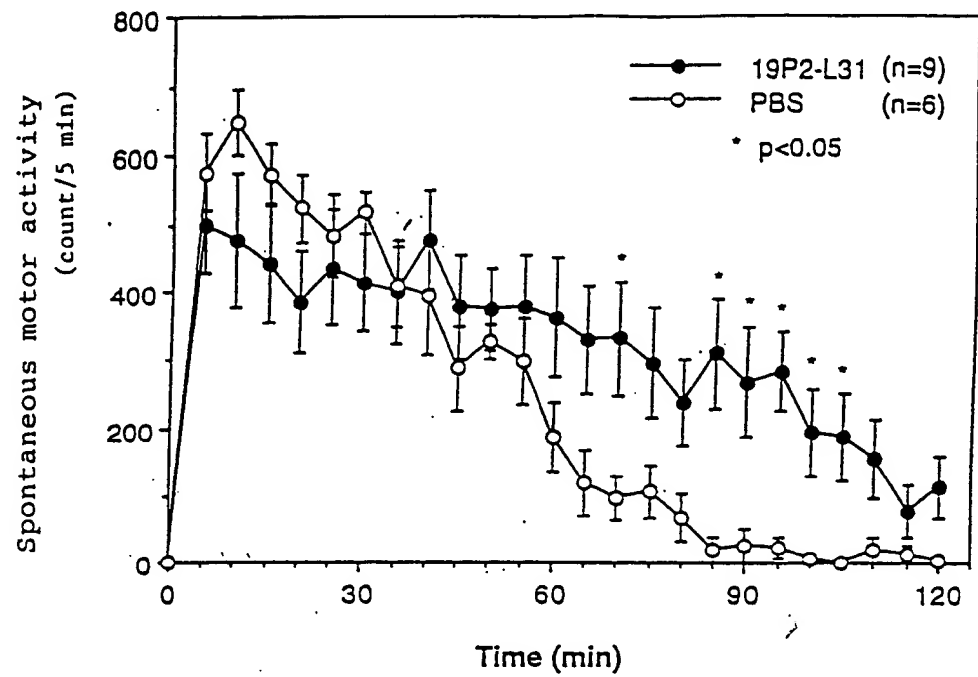


Fig. 41

(a)



(b)

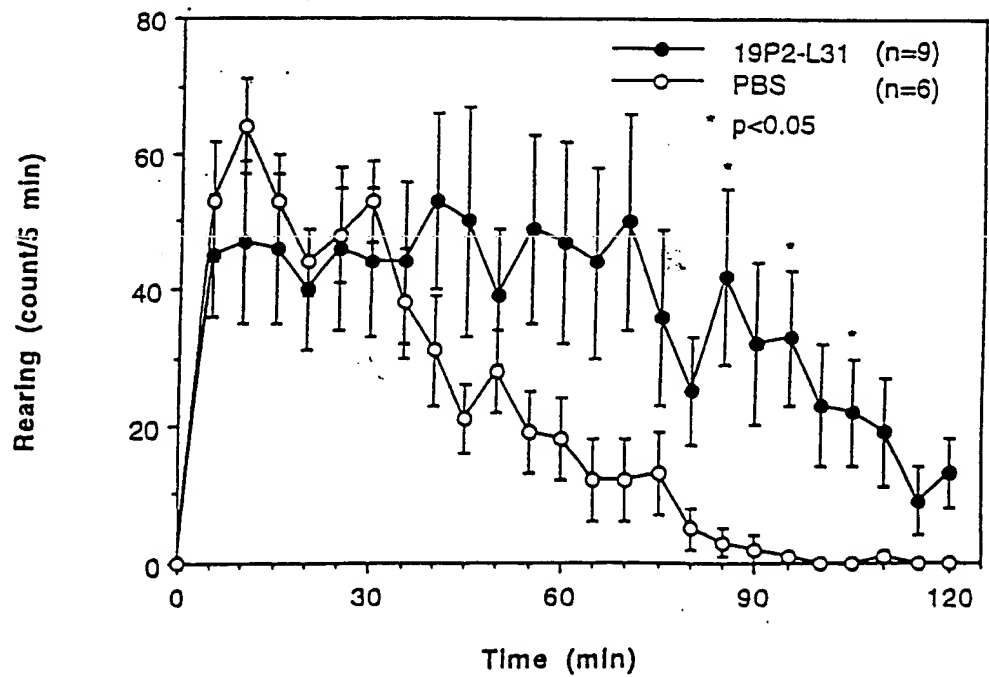
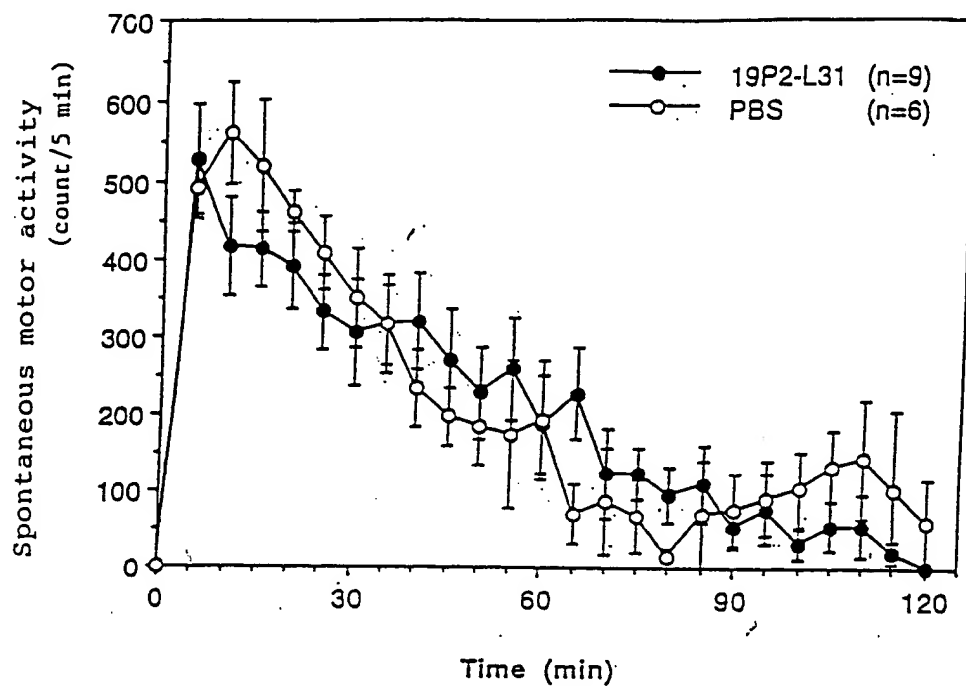


Fig. 42

(a)



(b)

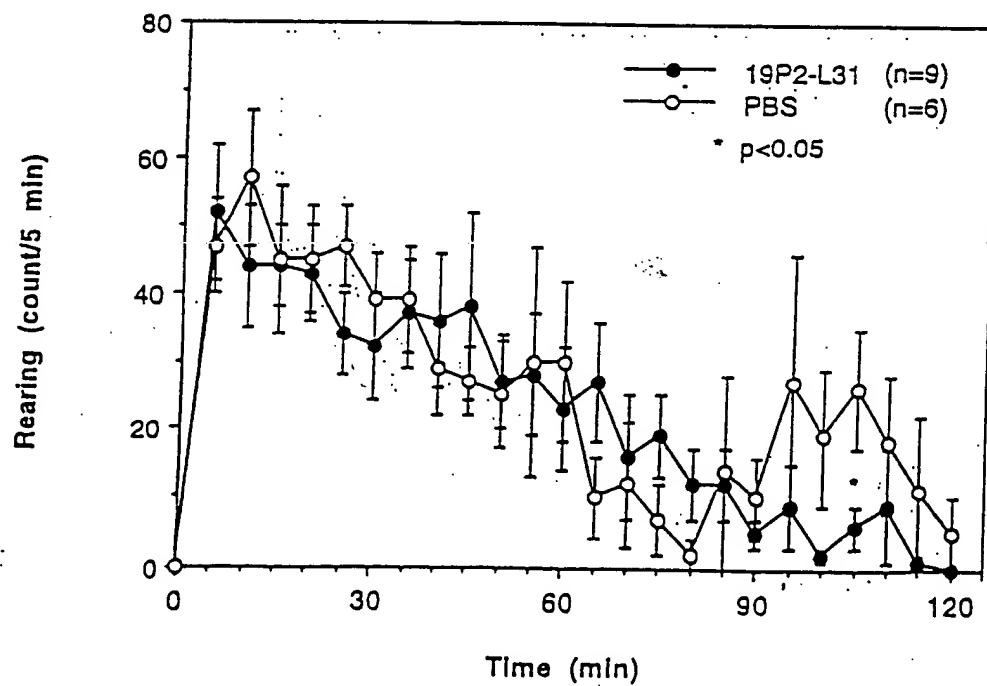
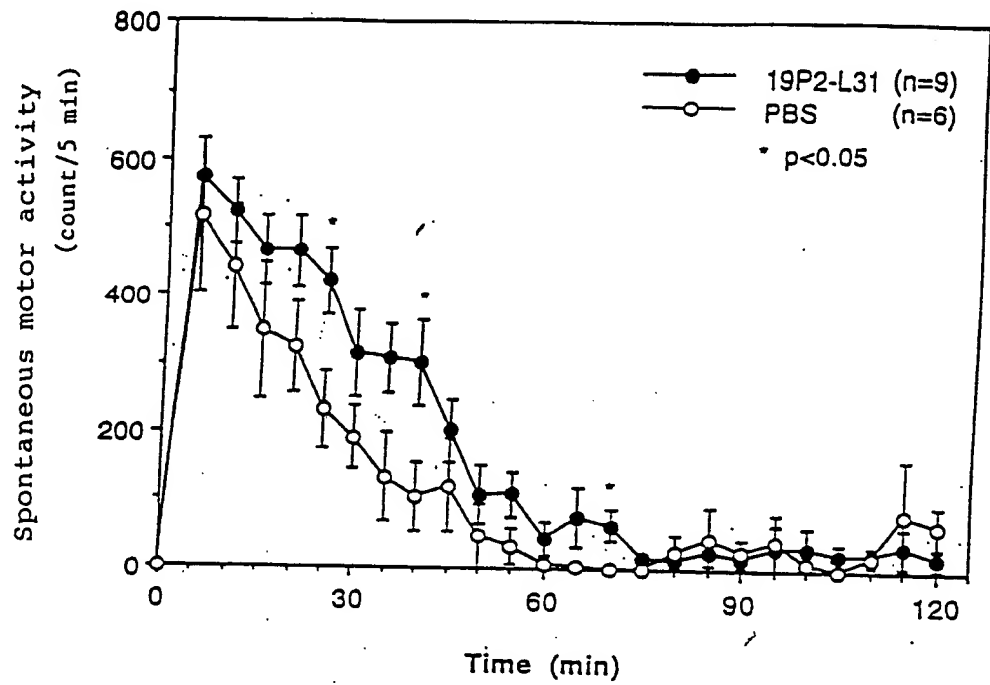


Fig. 43

(a)



(b)

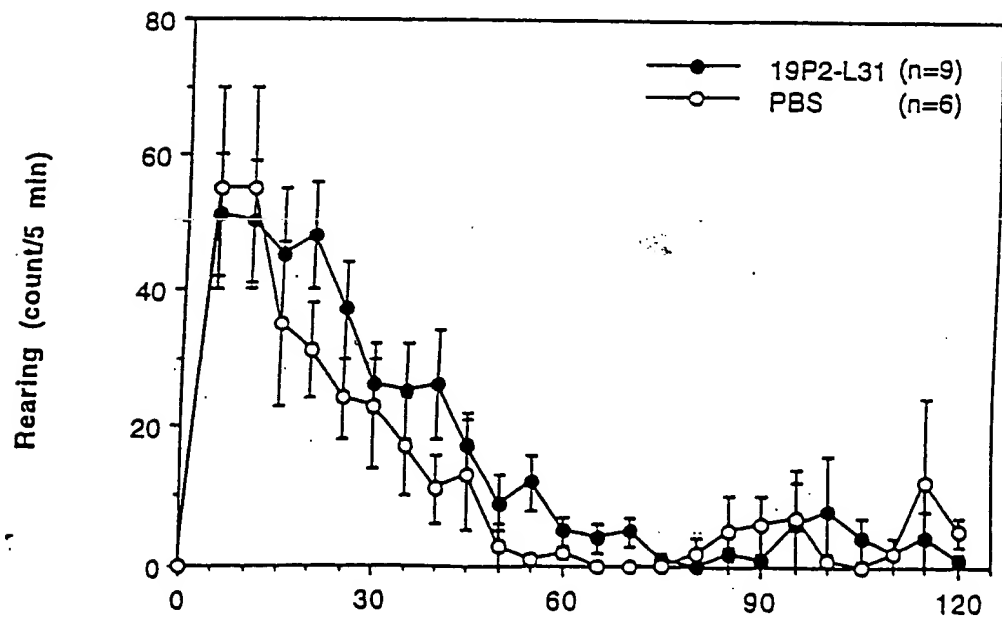
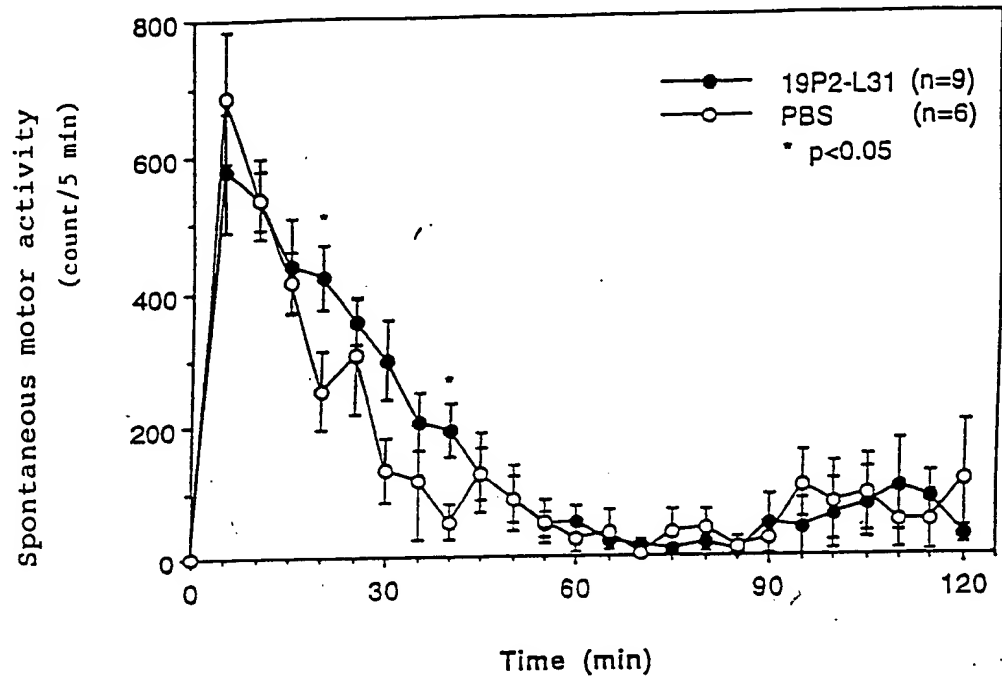


Fig. 44

(a)



(b)

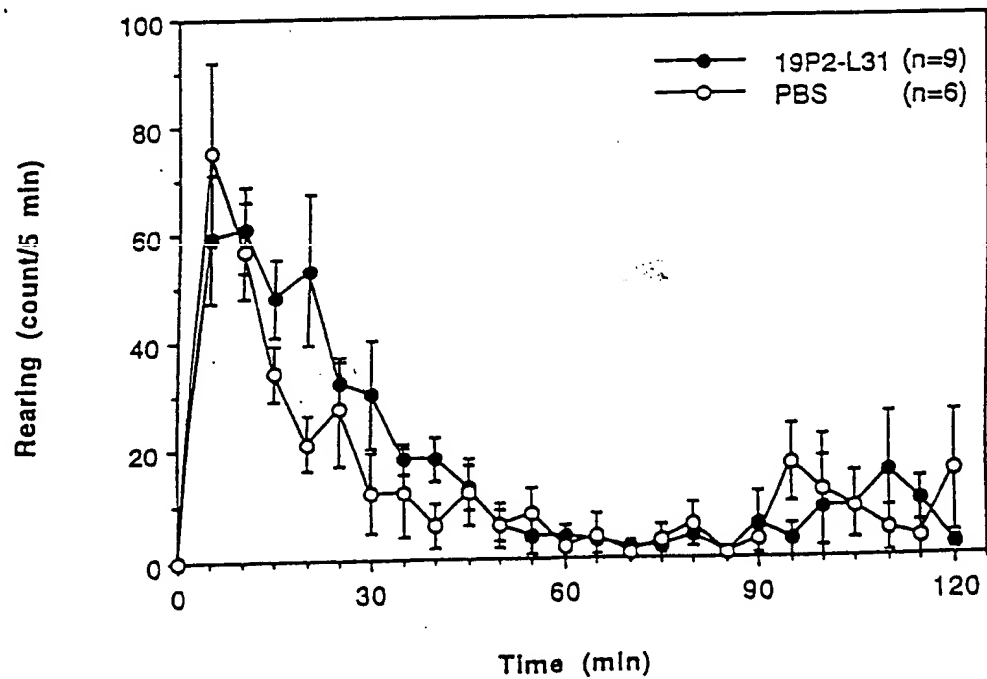


Fig. 45

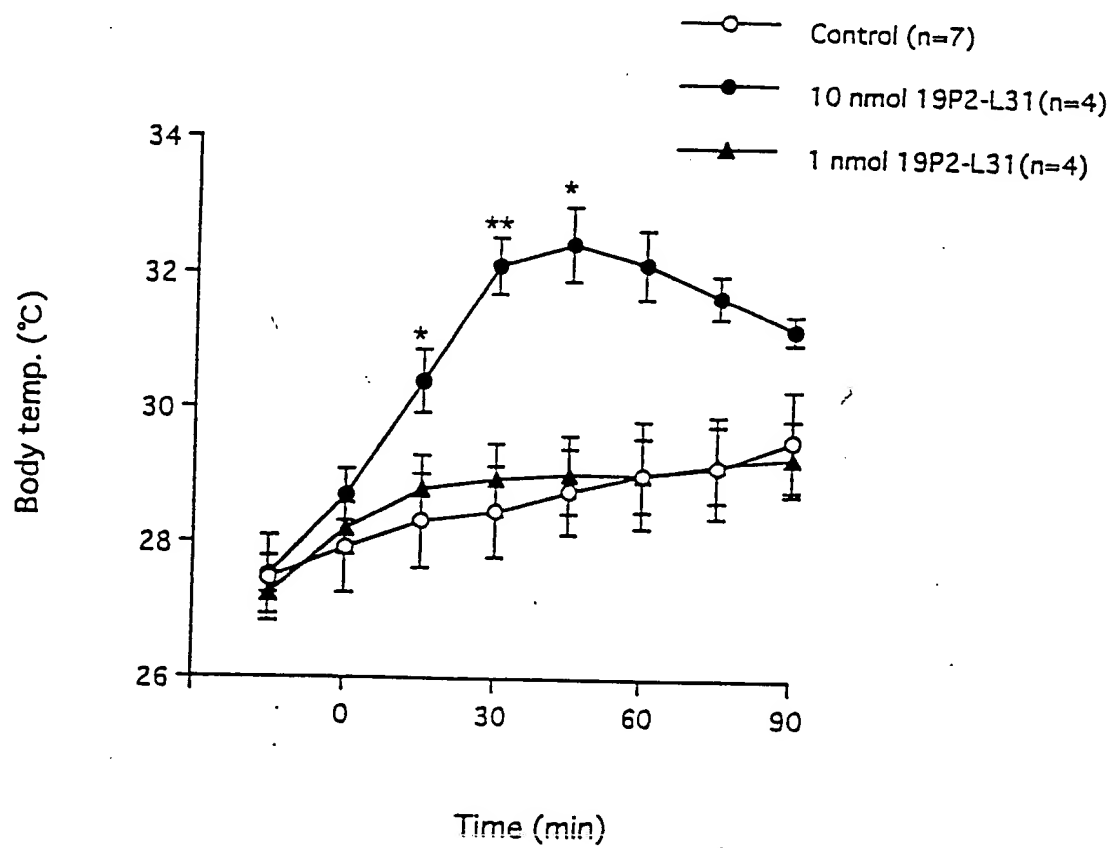
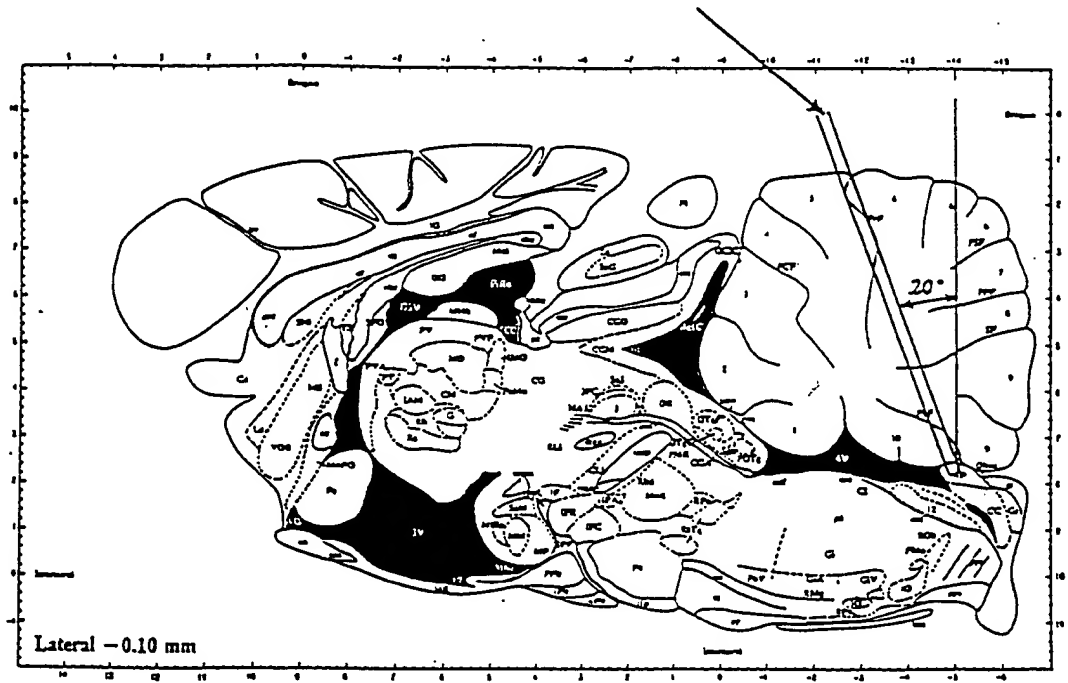
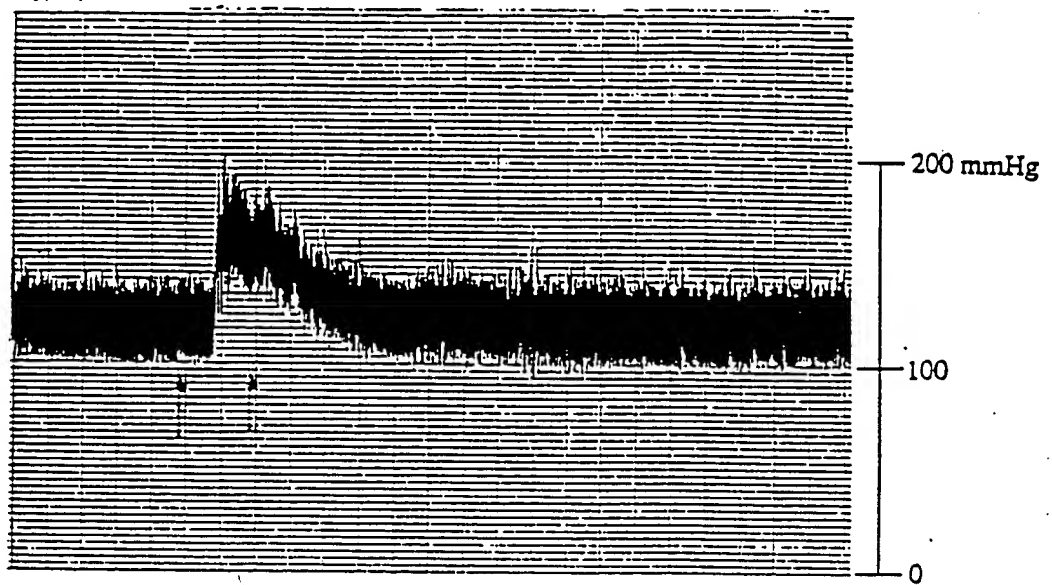


Fig. 46

micro-injection cannula



direct blood pressure



mean blood pressure

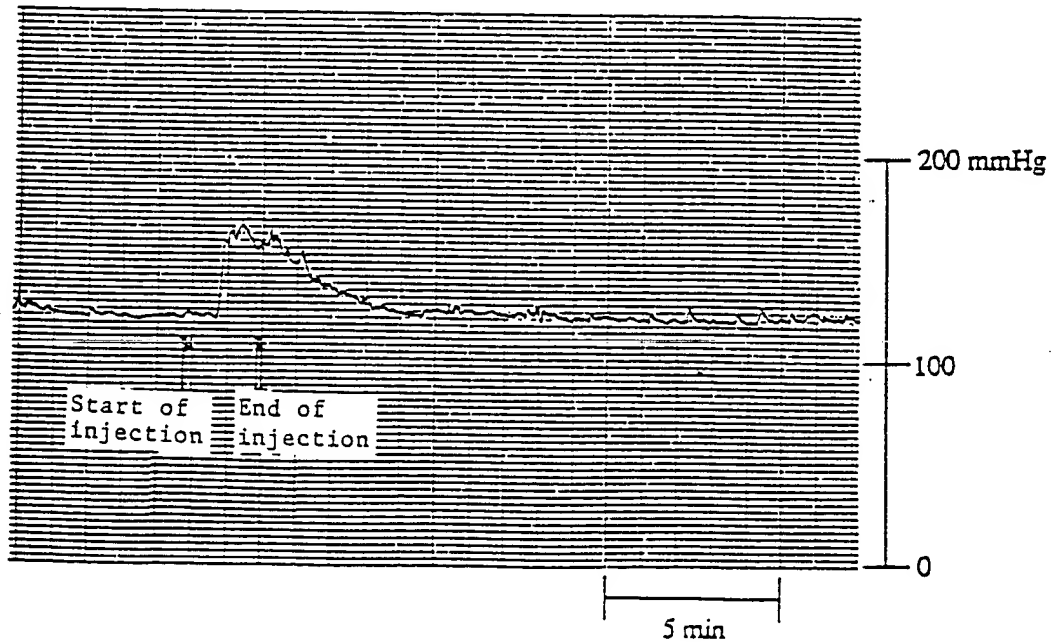


Fig. 48

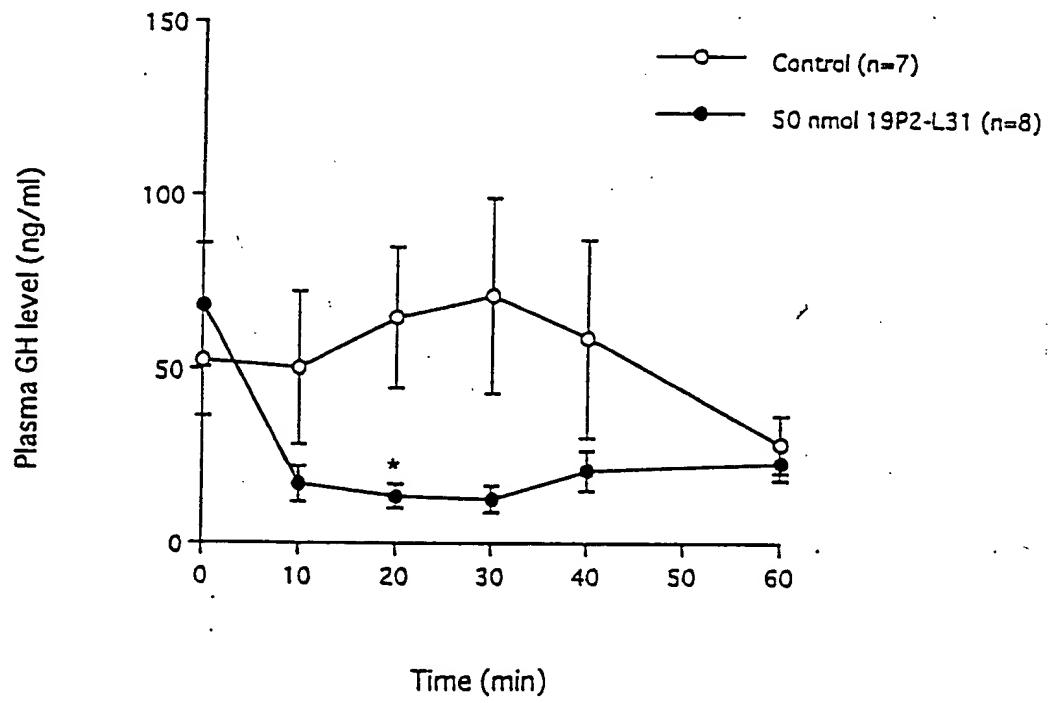


Fig. 49

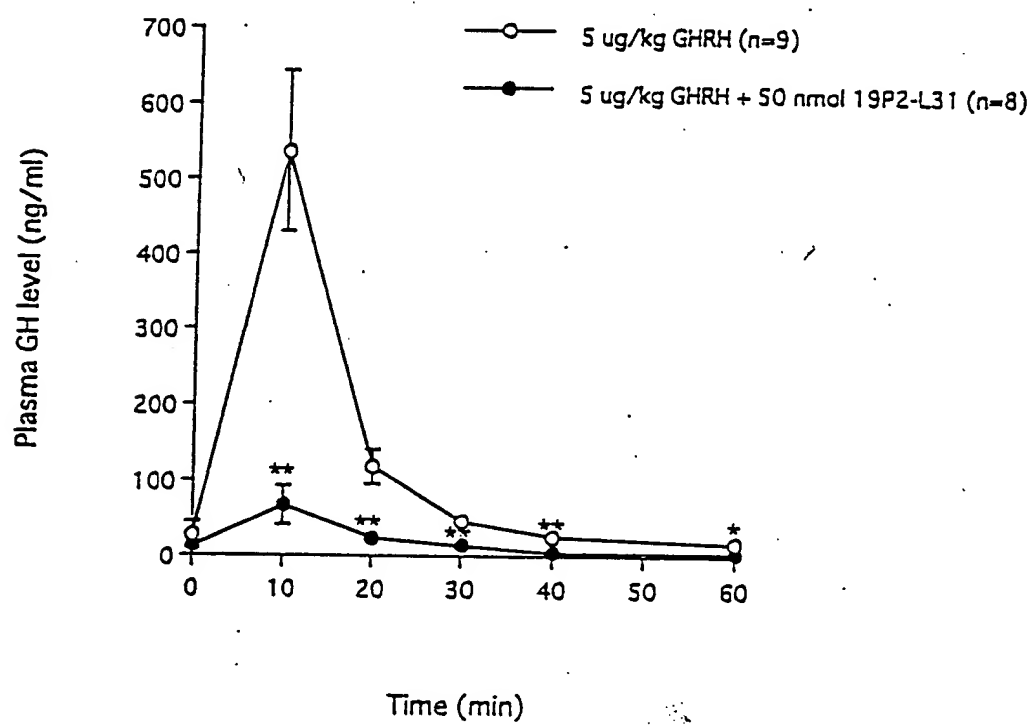


Fig. 50

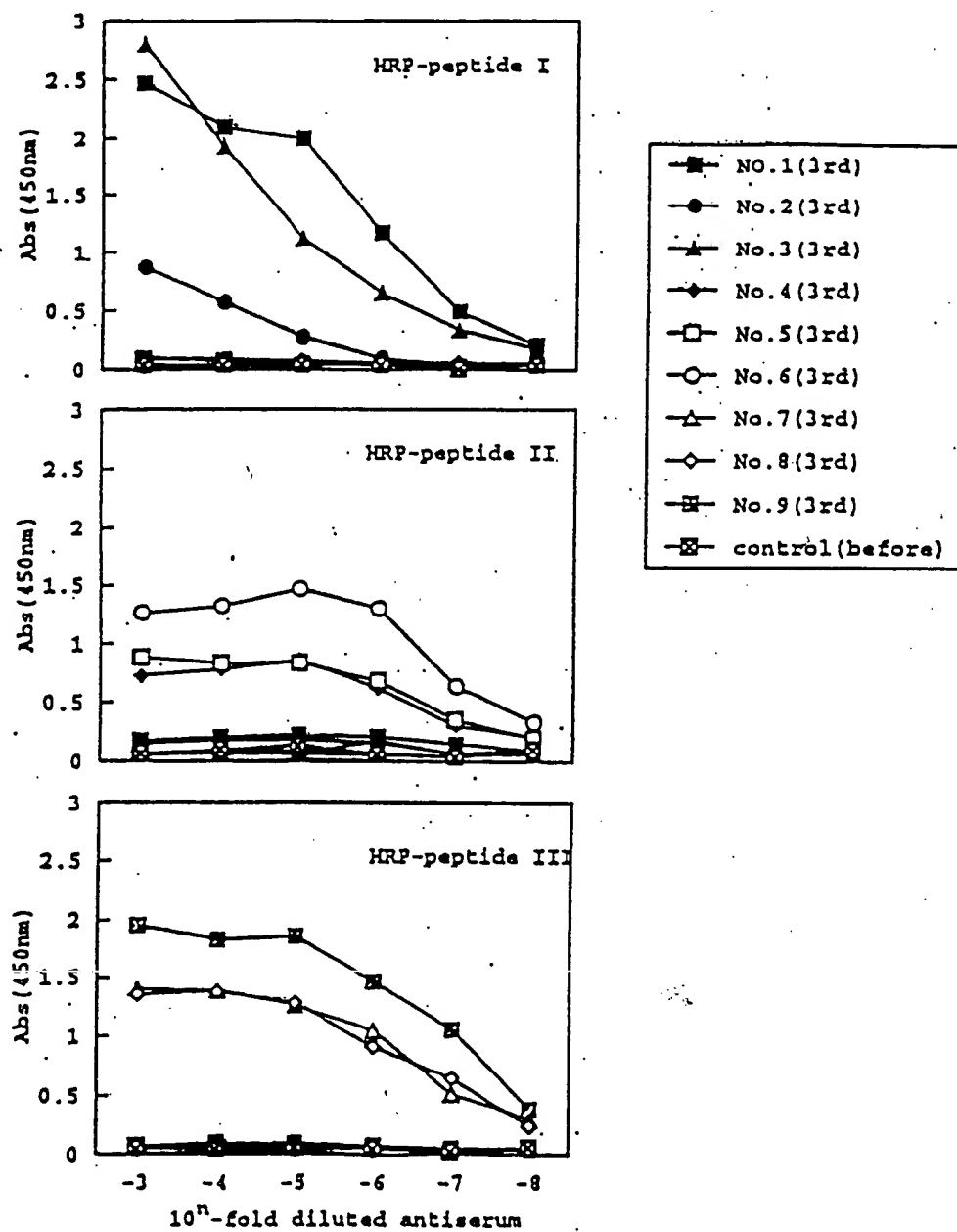
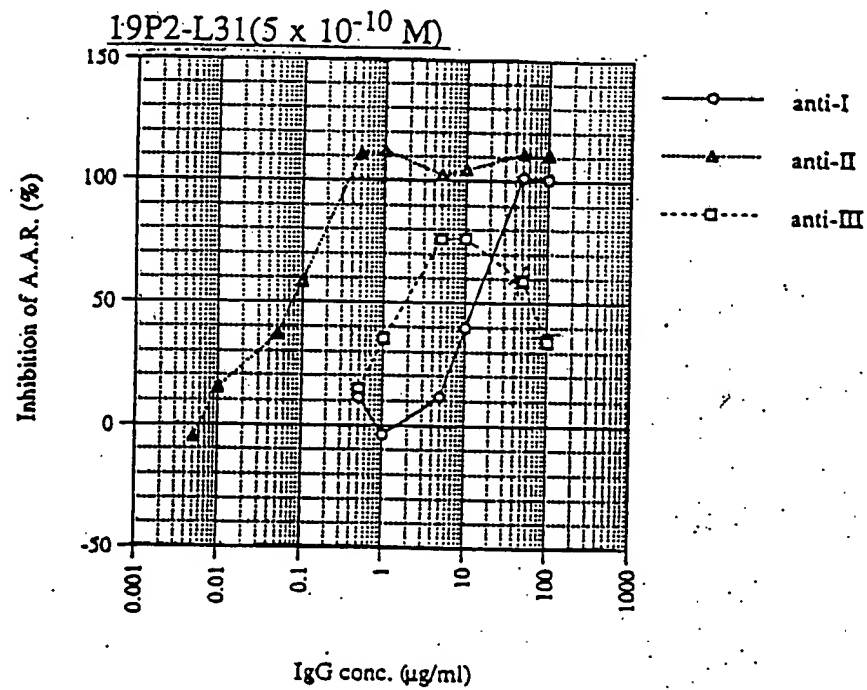


Fig. 51



000250" 06294560

	9	18	27	36	45	54
ASP ACT TCA CTG GCG	CCT GGA AGC ACT GGC	GCC GAG CAC GGG	GAT TTG TTT TGT GCG	CCC		
Nec Thr Ser Leu Pro	Pro Gly Thr Thr Gly Asp	Pro Asp Leu Phe Ser Gly Pro				
63	72	81	90	99	108	
TTC CCA CCC TTC ACT CCA GCC AAC CAG AGT GCA CAG OCT TCA CAG ACC AAT						
Ser Pro Ala Gly Ser Thr Pro Ala Asn Glu Ser Ala Glu Ala Ser Glu Ser Asn						
117	126	135	144	153	162	
GTC TCT GGC ACC GTT CGA CCA GCT GCA GTC ACT CCC TTC CAG ACC CTG CAA						
Val Ser Ala Thr Val Pro Arg Ala Ala Ala Val Thr Pro Phe Glu Ser Leu Glu						
171	180	189	198	207	216	
CDA GTC CAC CAG CTG AAG CCA CTG ATC GTG ARG CTG TAC ACC ATC CTC CTC GTC						
Leu Val His Glu Leu Lys Gly Leu Ile Val Met Leu Tyr Ser Ile Val Val Val						
225	234	243	252	261	270	
GTC GGT CTC GTG CCC AAC TCC CTG CTG CTG GTC GTC GTC GTC GTC GTC						
Val Gly Leu Val Gly Asn Cys Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg						
279	288	297	306	315	324	
CTG GC AAC GTC ACC AAC TTC CTC ATT CCC AAC CTG CCT TTG TCC GAT CTC CTC						
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu						
333	342	351	360	369	378	
ATG TCT GGC GGC TCT GTG CCT CTC ACC CTC CCC TAC CCC TTT GAA CCT GGT GGC						
Met Cys Ala Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly						
387	396	405	414	423	432	
TGC GTG TCT GGT GGA GGC CTC TCC CTA CCT GTT TTC TTC CAG CCC GTC ACC						
Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Glu Pro Val Thr						
441	450	459	468	477	486	
CTC TAC GGA TCC GTG TTC ACA CTC ACC ACA ATC CCT GTG GAC CCC TAT GTC GGT						
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val						
495	504	513	522	531	540	
CTG CTC CAC CCC CCA GGT GGC CCC ACC TCA CTC AAC CAC ACC ACC TAC CCC GTC						
Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Lys Leu Ser Ala Tyr Ala Val						
549	558	567	576	585	594	
CTG GGC AAC TCC GGT CCA TCT GCA CTC GTC GGC CCC CTC CCC CCC GTC CAC ACC						
Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr						
603	612	621	630	639	648	
TAC CAC GGA CAG CTC AAG CCC CC CAC CTC GTC CCC CTC TCT CAG CAG TTC TCC GGT						
Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly						
657	666	675	684	693	702	
TCT CAG CAG CCC CAG GGA CAG ACC TAC CCT TCC CCC CTC CTC GTC GTC ACC TAT						
Ser Glu Glu Arg Glu Arg Glu Ile Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr						
711	720	729	738	747	756	
TTC CTC CCC CTC CTC GGC ATT CTC CTC TCT TAC CTC CCC GTC TCC GTC AAG TTC						
Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu						
765	774	783	792	801	810	
CGC AAC CCC GTC GTC GGT GGC ACC GTC ACC CAC ACC CAC CCC CAC TCC CAC CCA						
Arg Asn Arg Val Val Pro Gly Ser Val Thr Glu Ser Glu Ala Asp Trp Asp Arg						
819	828	837	846	855	864	
GGC GGT GGC GGC ACC TTC TCC CTC CTC GTC GTC GTC GTC GTC GTC TTC CCC						
Ala Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala						
873	882	891	900	909	918	
GTC TCC TCC CTC CCT CTC CAC ATT TTC AAC CTG CTC CCC CAC CTG CAC CCC CCT						
Val Cys Trp Leu Pro Leu His Ile Phe Asn Leu Leu Arg Asp Leu Asp Pro Arg						
927	936	945	954	963	972	
CCC ATC CAC CCC TAC GGC TTC GGC GTC GTC CAG CTC CTC TCC CAC TCC CTT CCC						
Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Glu Leu Leu Cys His Trp Leu Ala						
981	990	999	1008	1017	1026	
ATG ACC TCC CCC TCC TAC AAC CCC TTC ATC TAT CCC TCC TCC CTC CAC CAC ACC TTC						
Nec Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Trp Leu His Asp Ser Phe						
1035	1044	1053	1062	1071	1080	
CCA GAG CAG CTA CCC AAC ATG GTC TCT TCT TCC CCC CCC AAG ACC GTG CCT CAC						
Arg Glu Glu Leu Arg Lys Met Leu Leu Ser Trp Pro Arg Lys Ile Val Pro His						
1089	1098	1107	1116			
CCC CAG AAT ATG ACC CTC AGT GTC GTC ATC TCA TCA J'						
Gly Glu Asn Met Thr Val Ser Val Val Ile						